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	First Inventor or Application Identifier	Ming-Ming Zhou
	Title	METHODS OF IDENTIFYING ...
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3. <input checked="" type="checkbox"/> Drawing(s) (35 U.S.C. 113) [Total Sheets 9]	ACCOMPANYING APPLICATION PARTS 7. <input type="checkbox"/> Assignment Papers (cover sheet & document(s)) 8. <input type="checkbox"/> 37 C.F.R. § 3.73(b) Statement <input type="checkbox"/> Power of Attorney (when there is an assignee) 9. <input type="checkbox"/> English Translation Document (if applicable) 10. <input type="checkbox"/> Information Disclosure Statement (IDS)/PTO-1449 <input type="checkbox"/> Copies of IDS Citations 11. <input type="checkbox"/> Preliminary Amendment 12. <input checked="" type="checkbox"/> Return Receipt Postcard (MPEP 503) (Should be specifically itemized) 13. <input type="checkbox"/> * Small Entity Statement(s) <input type="checkbox"/> Statement filed in prior application, Status still proper and desired (PTO/SB/09-12) 14. <input type="checkbox"/> Certified Copy of Priority Document(s) (if foreign priority is claimed) 15. <input checked="" type="checkbox"/> Other: atomic coordinates in 6 Tables	
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METHODS OF IDENTIFYING MODULATORS OF BROMODOMAINSFIELD OF THE INVENTION

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The present invention provides the three-dimensional structure of a histone acetyltransferase bromodomain. The three-dimensional structural information is included in the invention. The present invention also identifies for the first time, that bromodomains can bind to an acetylated binding partners. The interaction between bromodomains and their binding partners play a crucial role in various cellular functions, including in the regulation/modulation of DNA transcription. Therefore, the present invention provides procedures for identifying agents that can modulate the interaction of bromodomains and their binding partners by high throughput drug screening and/or through the use of rational drug design based on the three-dimensional data provided herein.

BACKGROUND OF THE INVENTION

In recent years great strides have been made in the elucidation of the steps involved in intercellular and intracellular signaling. Indeed, the individual steps of the cascade of events involved in a number of cellular signal transduction processes have been determined. For example, intercellular signal transduction generally begins with an intercellular ligand binding the extracellular portion of a receptor of the plasma membrane. The bound receptor then either directly or indirectly initiates the activation of one or more cellular factors. An activated cellular factor may act as transcription factor by entering the nucleus to interact with its corresponding genomic response element, or alternatively, it may interact with other cellular factors depending on the complexity of the process. In either case, one or more transcription factors ultimately bind to one or more specific genomic response elements. This binding plays a crucial role in the up and/or down regulation of the transcription of the specific genes that are under the control of these genomic response elements. However, the process of re-organizing the chromatin of eukaryotic cells, which is a prerequisite for the binding of the transcription factor to the genomic response elements, has remained a mystery.

- Chromatin contains several highly conserved histone proteins including: H3, H4, H2A, H2B, and H1. These histone proteins package eukaryotic DNA into repeating nucleosomal units that are folded into higher-order chromatin fibers [Luger and
- 5 Richmond, *Curr. Opin. Genet. Dev.* **8**:140-146 (1998)]. A portion of the histone that comprises roughly a quarter of the protein protrudes from the chromatin surface, and is thereby sensitive to proteolytic enzymes [van Holde, in *Chromatin* (Rich, A., ed., Springer, New York) pages111-148 (1988); Hect *et al.*, *Cell* **80**:583-592 (1995)].
- This portion of the histone is known as the “histone tail”. Histone tails tend to be free
- 10 for protein-protein interaction, and are also the portion of the histone most prone to post-translational modification. Such post-translational modification includes acetylation, phosphorylation, methylation, ubiquitination, and ADP-ribosylation [van Holde, in *Chromatin* (Rich, A., ed., Springer, New York) pages111-148 (1988)].
- 15 Of all classes of proteins, histones are amongst the most susceptible to post-translational modification. Perhaps the best studied post-translational modification of histones is the acetylation of specific lysine residues [Grunstin, M., *Nature*, **389**:349-352 (1997)]. Indeed, acetylation of histone lysine residues has been suggested to play a pivotal role in chromatin remodeling and gene activation. Consistently,
- 20 distinct classes of enzymes, namely histone acetyltransferases (HATs) and histone deacetylases (HDACs), acetylate or de-acetylate specific histone lysine residues [Struhl, *Genes Dev.* **12**:599-606 (1998)].
- Nearly all known nuclear HATs contain an approximately 110 amino acid sequence
- 25 known as the bromodomain [Jeanmougin *et al.*, *Trends in Biochemical Sciences*, **22**:151-153 (1997)], a protein motif that was initially discovered in *Drosophila* brahma protein. Bromodomains are found in a large number of chromatin-associated proteins and have now been identified in approximately 40 proteins, often adjacent to other protein motifs [Jeanmougin *et al.*, *Trends in Biochemical Sciences*, **22**:151-153
- 30 (1997); Tamkun *et al.*, *Cell*, **68**:561-572 (1992); Hanes *et al.*, *Nucleic Acids Research*, **20**:2603 (1992)]. Proteins that contain a bromodomain often contain a second bromodomain. However, despite the wide occurrence of bromodomains and their

likely role in chromatin regulation, their three-dimensional structure and binding partners heretofore have remained unknown.

Therefore, there is a need to identify a binding partner for a bromodomain. In addition, there is a need to identify agonists or antagonists to the bromodomain-binding partner complex. Since a preferred method of drug-screening relies on structure based drug design, there is also a need to determine the three-dimensional structure of a bromodomain. In this case, once the three dimensional structure of bromodomain is determined, potential agonists and/or potential antagonists can be designed with the aid of computer modeling [Bugg *et al.*, *Scientific American*, Dec.:92-98 (1993); West *et al.*, *TIPS*, 16:67-74 (1995); Dunbrack *et al.*, *Folding & Design*, 2:27-42 (1997)]. However, heretofore the three-dimensional structure of the bromodomain has remained unknown. Therefore, there is a need for obtaining a form of the bromodomain that is amenable for NMR analysis and/or X-ray crystallographic analysis. Furthermore, there is a need for the determination of the three-dimensional structure of the bromodomain. Finally, there is a need for procedures for related structural based drug design predicated on such structural data.

The citation of any reference herein should not be construed as an admission that such reference is available as "Prior Art" to the instant application.

SUMMARY OF THE INVENTION

The present invention provides, for the first time, that bromodomains bind to acetyl-lysine residues of proteins. The present invention also provides the three-dimensional structure of a bromodomain as well as the three-dimensional structure of a bromodomain-acetyl-histamine complex. The structural information provided can be employed in methods of identifying drugs that can modulate the cellular processes that involve bromodomain-acetyl-lysine interactions. These interactions include chromatin remodeling, which is a required step in eukaryotic transcription. In a particular embodiment, the three-dimensional structural information is used in the design of an inhibitor of leukemia.

The present invention provides an isolated nucleic acid that encodes a peptide consisting of about 21 to 40 amino acids that comprises a ZA loop of a bromodomain. In a preferred embodiment the peptide comprises about 23 to 34 amino acids. The isolated nucleic acid can further comprise a heterologous nucleotide sequence.

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In a preferred embodiment the peptide comprises the amino acid sequence of SEQ ID NO:3. In another embodiment the peptide comprises the amino acid sequence of SEQ ID NO:43. In particular embodiments the ZA loop is obtained from the bromodomain having the amino acid sequence of SEQ ID NO:7, or SEQ ID NO:8, or SEQ ID NO:9, or SEQ ID NO:10, or SEQ ID NO:11, or SEQ ID NO:12, or SEQ ID NO:13, or SEQ ID NO:14, or SEQ ID NO:15, or SEQ ID NO:16, or SEQ ID NO:17, or SEQ ID NO:18, or SEQ ID NO:19, or SEQ ID NO:20, or SEQ ID NO:21, or SEQ ID NO: 22, or SEQ ID NO:23, or SEQ ID NO:24, or SEQ ID NO:25, or SEQ ID NO:26, or SEQ ID NO:27, or SEQ ID NO:28, or SEQ ID NO:29, or SEQ ID NO:30, or SEQ ID NO: or SEQ ID NO:31, or SEQ ID NO:32, or SEQ ID NO: 33, or SEQ ID NO:34, or SEQ ID NO:35, or SEQ ID NO:36 , or SEQ ID NO:37, or SEQ ID NO:38, or SEQ ID NO: or SEQ ID NO:39, or SEQ ID NO:40, or SEQ ID NO:41, or SEQ ID NO:42.

The present invention further provides a recombinant DNA molecule that comprises an isolated nucleic acid of the present invention, as described above, with or without a heterologous nucleotide sequence. Such a recombinant DNA molecule can be operatively linked to an expression control sequence and can be part of an expression vector. The present invention further provides a cell that comprises such an expression vector. The cell can be either a eukaryotic or a prokaryotic cell. The present invention further provides a method of expressing the peptides of the present invention or fragments thereof in this cell. One such method comprises culturing the cell in an appropriate cell culture medium under conditions that provide for expression of the peptide by the cell.

The present invention further provides a peptide consisting of about 21 to 40 amino acids that comprises a ZA loop of a bromodomain. In a preferred embodiment the

peptide comprises about 23 to 34 amino acids. The present invention also provides fusion proteins or peptides comprising these peptides.

In a preferred embodiment the peptide comprises the amino acid sequence of SEQ ID NO:3. In another embodiment the peptide comprises the amino acid sequence of SEQ ID NO:43. In particular embodiments the ZA loop is obtained from the bromodomain having the amino acid sequence of SEQ ID NO:7, or SEQ ID NO:8, or SEQ ID NO:9, or SEQ ID NO:10, or SEQ ID NO:11, or SEQ ID NO:12, or SEQ ID NO:13, or SEQ ID NO:14, or SEQ ID NO:15, or SEQ ID NO:16, or SEQ ID NO:17, or SEQ ID NO:18, or SEQ ID NO:19, or SEQ ID NO:20, or SEQ ID NO:21, or SEQ ID NO: 22, or SEQ ID NO:23, or SEQ ID NO:24, or SEQ ID NO:25, or SEQ ID NO:26, or SEQ ID NO:27, or SEQ ID NO:28, or SEQ ID NO:29, or SEQ ID NO:30, or SEQ ID NO: or SEQ ID NO:31, or SEQ ID NO:32, or SEQ ID NO: 33, or SEQ ID NO:34, or SEQ ID NO:35, or SEQ ID NO:36 , or SEQ ID NO:37, or SEQ ID NO:38, or SEQ ID NO: or SEQ ID NO:39, or SEQ ID NO:40, or SEQ ID NO:41, or SEQ ID NO:42.

The present invention also provides antibodies raised against the peptides/proteins of the present invention, or raised against an antigenic fragment of these proteins/fragments. In a particular embodiment an antibody is raised against a fragment of the ZA loop of a bromodomain. In another embodiment an antibody is raised against a fragment of a protein or peptide that comprises an acetyl-lysine, wherein the protein or peptide can bind to a bromodomain. Such fragments can be conjugated to a carrier protein or be part of a fusion protein. In one embodiment the antibody is a polyclonal antibody. In another embodiment, the antibody is a monoclonal antibody. A hybridoma that makes the monoclonal antibody is also part of the present invention. In a particular embodiment the antibody is a chimeric antibody. Antibodies that can specifically recognize acetyl-lysine residues involved bromodomain binding are also part of the present invention.

In another aspect of the present invention a method is provided for identifying a compound that modulates the affinity of a bromodomain for a ligand (and/or protein) that comprises an acetylated lysine. One such embodiment comprises contacting the

bromodomain and the ligand in the presence of a compound under conditions that ,
the bromodomain and the ligand bind in the absence of the compound. The affinity of
the bromodomain for the ligand is then determined (*e.g.*, measured). A compound is
identified as a compound that modulates the affinity of the bromodomain for the
5 ligand when there is a change in the affinity of the bromodomain for the ligand in the
presence of the compound. When the affinity of the bromodomain for the ligand
increases in the presence of the compound, the compound is identified as a promoting
agent for the bromodomain-ligand complex. When the affinity of the bromodomain
for the ligand decreases in the presence of the compound, the compound is identified
10 as an inhibitor of the bromodomain-ligand complex. In a preferred embodiment, the
compound to be tested is pre-selected by performing rational drug design with the set
of atomic coordinates obtained from one or more of Tables 1-6. More preferably the
selecting is performed in conjunction with computer modeling. In a particular
embodiment, the compound is selected by performing rational drug design with the
15 set of atomic coordinates obtained from a set of atomic coordinates defining the three-
dimensional structure of a bromodomain consisting of the amino acid sequence of
SEQ ID NO:7 alone or with acetyl-histamine.

The present invention also provides a method of identifying a compound that
20 modulates the stability of a bromodomain-acetyl-lysine binding complex. One such
embodiment comprises contacting the bromodomain-acetyl-lysine binding complex in
the presence of the compound under conditions in which the bromodomain-acetyl-
lysine binding complex forms in the absence of the compound. The stability of the
bromodomain-acetyl-lysine binding complex is then determined (*e.g.*, measured). A
25 compound is identified as a compound that modulates the stability of the
bromodomain-acetyl-lysine binding complex, when there is a change in the stability
of the bromodomain-acetyl-lysine binding complex in the presence of that compound.
When the stability of the bromodomain-acetyl-lysine binding complex increases in the
presence of the compound, the compound is identified as a stabilizing agent. When
30 the stability of the bromodomain-acetyl-lysine binding complex decreases in the
presence of the compound, the compound is identified as an inhibitor. In a preferred
embodiment, the compound to be tested is pre-selected by performing rational drug

design with the set of atomic coordinates obtained from one or more of Tables 1-6. More preferably the selecting is performed in conjunction with computer modeling. In a particular embodiment, the compound is selected by performing rational drug design with the set of atomic coordinates obtained from a set of atomic coordinates
 5 defining the three-dimensional structure of a bromodomain consisting of the amino acid sequence of SEQ ID NO:7 alone or with acetyl-histamine.

As anyone having skill in the art of drug development would readily understand, the potential drugs selected by the above methodologies can be refined by re-testing in
 10 appropriate drug assays, including those disclosed herein. Chemical analogs of such potential drugs can be obtained (either through chemical synthesis or drug libraries) and be analogously tested. Therefore, methods comprising successive iterations of the steps of the individual drug assays, as exemplified herein, using either repetitive or different binding studies, or transcription activation studies or other such studies are
 15 envisioned in the present invention. In addition, potential drugs may be identified first by rapid throughput drug screening, as described below, prior to performing computer modeling on a potential drug using the three-dimensional structure of the bromodomain.

20 The present invention further comprises all of the potential, selected, and putative compounds (drugs) identified by the methods of the present invention, as well as the final drugs themselves identified with the methods of the present invention.

The present invention further provides a method for identifying a potential binding
 25 partner for a protein (*e.g.*, a histone) comprising an acetyl-lysine. One such embodiment comprises contacting the protein with a polypeptide comprising a bromodomain. In a preferred embodiment the bromodomain comprises the amino acid sequence of SEQ ID NO:3. In particular embodiments the bromodomain has the amino acid sequence of SEQ ID NO:7, or SEQ ID NO:8, or SEQ ID NO:9, or SEQ ID
 30 NO:10, or SEQ ID NO:11, or SEQ ID NO:12, or SEQ ID NO:13, or SEQ ID NO:14, or SEQ ID NO:15, or SEQ ID NO:16, or SEQ ID NO:17, or SEQ ID NO:18, or SEQ ID NO:19, or SEQ ID NO:20, or SEQ ID NO:21, or SEQ ID NO: 22, or SEQ ID

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It is a further object of the present invention to provide an assay for identifying proteins that contain bromodomains that bind proteins that comprise acetyl-lysine.

It is a further object of the present invention to provide methods of identifying drugs that can inhibit the binding of a bromodomain to a protein containing acetyl-lysine.

10 It is a further object of the present invention to provide a method of identifying drugs
that can treat leukemia.

15 These and other aspects of the present invention will be better appreciated by
reference to the following drawings and Detailed Description.

Figure 1. Structure-based sequence alignment of a selected number of bromodomains. The sequences were aligned based on the NMR-derived structure of the P/CAF bromodomain, and the predicated four α -helices are shown in green boxes. Bromodomains are grouped on the basis of the sequence and/or functional similarities as described by Jeanmougin *et al.*, [Trends in Biochemical Sciences, **22**:151-153 (1997)]. Residue numbers of the P/CAF bromodomain are indicated above its sequence. Three absolutely conserved residues, corresponding to Pro751, Pro767, and Asn803 in the P/CAF bromodomain, are shown in red. Highly conserved residues are colored in blue. The residues of the P/CAF bromodomain that interact with acetyl-histamine, as determined by intermolecular NOEs, are indicated by asterisks. The ZA loop, which is critical for acetyl-lysine binding, for each of the indicated bromodomains is also identified. The underlined residues were changed individually

by site-directed mutagenesis to Ala. Genbank accession numbers for the proteins are as indicated in Table 8, in the Example below, along with the SEQ ID NOs. for the bromodomain sequences.

- 5 Figures 2A-2H depict the structure of the P/CAF bromodomain. Figures 2A-2B shows the stereoview of the C_α trace of 30 superimposed NMR-derived structures of the bromodomain (residues 722-830). The N-terminal four residues (SKEP) which are structurally disordered are omitted for clarity. For the final 30 structures, the root-mean-square deviations (RMSDs) of the backbone and all heavy atoms are $0.63 \pm 0.11 \text{ \AA}$ and $1.15 \pm 0.12 \text{ \AA}$ for residues 723-830, respectively. The RMSDs of the backbone and all heavy atoms for the four α -helices (residues 727-743, 770-776, 785-802, and 807-827), are $0.34 \pm 0.04 \text{ \AA}$ and $0.87 \pm 0.06 \text{ \AA}$, respectively. Figures 2C-2D show the stereoview of the bromodomain structures from the bottom of the protein, which is rotated approximately 90° from the orientation in Figures 2A-2B.
- 10 $\pm 0.11 \text{ \AA}$ and $1.15 \pm 0.12 \text{ \AA}$ for residues 723-830, respectively. The RMSDs of the backbone and all heavy atoms for the four α -helices (residues 727-743, 770-776, 785-802, and 807-827), are $0.34 \pm 0.04 \text{ \AA}$ and $0.87 \pm 0.06 \text{ \AA}$, respectively. Figures 2C-2D show the stereoview of the bromodomain structures from the bottom of the protein, which is rotated approximately 90° from the orientation in Figures 2A-2B.
- 15 Figure 2E shows the Ribbons [Carson, M., *J. Appl. Crystallogr.* **24**:958-961 (1991)] depiction of the averaged minimized NMR structure of the P/CAF bromodomain. The orientation of Figure 2E is as shown in Figures 2A-2B. Figures 2F-2G are schematic representations of the overall topology of the up-and-down four-helix bundle folds with the opposite handedness. The left-handed fold is seen in bromodomain, cytochrome b_5 , and T4 lysozyme (left, Figure 2F), whereas the right-handed four-helix bundles are observed in proteins such as hemerythrin and cytochrome b_{562} (right, Figure 2G) [Richardson, J., *Adv. Protein Chem.*, **34**:167-339 (1989); Presnell and Cohen, *Proc. Natl. Acad. Sci. USA* **86**:6592-6596 (1989)].
- 20 bromodomain, cytochrome b_5 , and T4 lysozyme (left, Figure 2F), whereas the right-handed four-helix bundles are observed in proteins such as hemerythrin and cytochrome b_{562} (right, Figure 2G) [Richardson, J., *Adv. Protein Chem.*, **34**:167-339 (1989); Presnell and Cohen, *Proc. Natl. Acad. Sci. USA* **86**:6592-6596 (1989)].
- Figure 2H is a molecular surface representation of the electrostatic potential (blue = positive; red = negative) of the bromodomain calculated in GRASP [Nicholls *et al.*, *Biophys. J.* **64**:166-170 (1993)]. The hydrophobic and aromatic residues (Tyr809, Tyr802, Tyr760, Ala757, and Val752) located between the ZA and BC loops are indicated.
- 25 positive; red = negative) of the bromodomain calculated in GRASP [Nicholls *et al.*, *Biophys. J.* **64**:166-170 (1993)]. The hydrophobic and aromatic residues (Tyr809, Tyr802, Tyr760, Ala757, and Val752) located between the ZA and BC loops are indicated.
- 30 Figures 3A-3C show the binding of the P/CAF bromodomain to AcK. Figure 3A shows the superimposed region of the 2D ^{15}N -HSQC spectra of the bromodomain (approximately 0.5 mM) in its free form (red) and complexed to the AcK-containing

H4 peptide (molar ratio 1:6) (black). Figure 3B is the Ribbon and dotted-surface diagram of the bromodomain depicting the location of the lysine-acetylated H4 peptide binding site. The color coding reflects the chemical shift changes ($\Delta\delta$) of the backbone amide ^1H and ^{15}N resonances upon binding to the AcK peptide as observed in the ^{15}N -HSQC spectra. The normalized weighted average of the chemical shift changes was calculated by $\Delta_{av}/\Delta_{max} = [\Delta\delta_{\text{NH}}^2 + \Delta\delta_{\text{N}}^2/25]/2]^{1/2}/\Delta_{max}$, where Δ_{max} is the maximum weighted chemical shift difference observed for Tyr809 (0.16ppm). The backbone atoms are color-coded in red, yellow, or green for residues that have Δ_{av}/Δ_{max} of >0.6 (Tyr809, Glu808, Asn803, and Ala757), $0.2-0.6$ (Ala813, Tyr802, Tyr760, and Val752), or <0.2 (Cys812, Ser807, Cys799, Phe796, and Phe748), respectively. The non-perturbed residues are shown in blue. Figure 3C shows the chemical structures of acetyl-lysine, acetyl-histamine, and acetyl-histidine.

Figure 4 depicts the acetyl-lysine binding pocket. This is the Ribbons [Carson, M., *J. Appl. Crystallogr.* **24**:958-961 (1991)] depiction of a portion of the P/CAF bromodomain complexed with the acetyl-histamine. The ligand is color-coded by atom type.

DETAILED DESCRIPTION OF THE INVENTION

The present invention identifies a general binding partner (ligand) for the protein motif known as the bromodomain. Indeed, by combining structural and site-directed mutagenesis studies the present invention demonstrates that bromodomains can interact specifically with acetyl-lysine (AcK), making them the first protein modules known to exhibit such interactions. Like other modular domains, such as Src homology-2 (SH2) and phosphotyrosine binding (PTB) domains, which specifically interact with phosphotyrosine-containing proteins, the bromodomain/acetyl-lysine recognition provides a means to regulate protein-protein interactions via protein lysine acetylation. The nature of the acetyl-lysine recognition by the bromodomain is similar to that of histone acetyltransferase interaction with acetyl-CoA. The present invention therefore couples for the first time, the functionality of the bromodomain with the HAT activity of coactivators in the regulation of gene transcription.

The present invention further provides both a nuclear magnetic resonance (NMR) structure of the bromodomain from the HAT coactivator P/CAF (p300/CBP-associated factor) as well as the structure for the P/CAF bromodomain in complex with acetyl-histamine. The structure reveals an unusual left-handed up-and-down four-helix bundle.

The results disclosed herein explain prior deletion experiments which showed that the bromodomain is indispensable for the function of GCN5 in yeast.

Bromodomain-AcK binding also appears to be important for the assembly and activity of multiprotein complexes in transcriptional activation. The results reported herein therefore, form the foundation for identifying specific biological ligands and for defining the molecular mechanisms by which the extensive family of bromodomains participate in chromatin remodeling and transcriptional activation

As disclosed herein, the binding partner for the bromodomain is a peptide or protein comprising an acetyl-lysine (AcK). Interestingly, whereas a free acetyl-lysine does not appear to bind the bromodomain, an analog of the acetyl-lysine, acetyl-histamine, does. This is most likely due to the additional charge present in the free amino acid. Consistently, free acetyl-histidine also does not to bind the bromodomain.

The present invention further provides a key region of the bromodomain for the interaction with its acetyl-lysine binding partner, the ZA loop. The amino acid sequence of the ZA loop is defined in Figure 1 for a number of bromodomains and is depicted in Figure 2A for P/CAF. In a particular embodiment, the ZA loop has between about 21 and 40 amino acid residues comprising the amino acid sequence of :

F X₂₋₃ P X₅₋₈ J_{P/K/H} X Y J_{Y/F/H} X₅ P J_{M/I/V} D (SEQ ID NO:3)

more preferably the ZA loop has about 23 to 34 amino acid residues and comprises the amino acid sequence:

X₂ F X₂₋₃ P X₅₋₈ J_{P/K/H} X Y J_{Y/F/H} X₅ P J_{M/I/V} D (SEQ ID NO:43)

(1) The single letter amino acid code is used in this description, *i.e.*, “F” for phenylalanine; “P” for proline; “Y” for tyrosine; and “D” for aspartic acid.

(2) “X” indicates any amino acid (an undesignated amino acid); and X, X₂, X₂₋₃, X₅, and X₅₋₈ indicates one undesignated amino acid, two consecutive undesignated amino acids, two or three consecutive undesignated amino acids, five consecutive undesignated amino acids, and five to eight consecutive undesignated amino acids respectively.

(3) “J” indicates that identity of the amino acid is restricted to a particular group, again the one letter code is used

- 10 : (i) J_{P/K/H} is either proline, lysine or histidine.
 (ii) J_{Y/F/H} is either tyrosine, phenylalanine or histidine.
 (iii) J_{M/I/V} is either methionine, isoleucine, or valine.

Since this region of the bromodomain is important in binding its acetyl-lysine binding partner, antibodies specifically raised against this region are also included in the present invention. In a particular embodiment, the antibody is a humanized chimeric antibody that can be used in therapeutic treatment. Thus monoclonal, chimeric, and polyclonal antibodies raised against bromodomains, preferably against amino acid residues in the ZA loop region are part of the present invention. In a specific embodiment the antibody is raised against a peptide, fusion peptide or conjugated peptide consisting of amino acid residues 746 to 765 of SEQ ID NO:2, *i.e.*, WPFMEPVKRTEAPGYEYEVIR (SEQ ID NO:44). Such antibodies can be used in the treatment of leukemia for example. Alternatively, these antibodies can be used in drug discovery assays.

25 Thus the present invention provides the first detailed structural information regarding a bromodomain and a bromodomain complexed with its acetylated binding partner. The present invention therefore provides the three-dimensional structure of the bromodomain and a bromodomain acetylated binding partner complex. Since the interaction of the bromodomain with a histone for example, can play a significant role in chromatin remodeling/regulation, the structural information provided herein can be employed in methods of identifying drugs that can modulate basic cell processes by modulating the transcription. In a particular embodiment, the three-dimensional

Indeed, the bromodomain and lysine-acetylated protein interaction can now be

5 implicated to play a causal role in the development of a number of diseases including
cancers such as leukemia. For example, chromatin remodeling plays a central role in
the etiology of viral infection and cancer [Archer and Hodin, *Curr. Opin. Genet. Biol.*
9:171-174 (1999); Jacobson and Pillus, *Curr. Opin. Genet. Biol.* 9:175-184 (1999)].
Both altered histone acetylation/deacetylation and aberrant forms of chromatin-
10 remodeling complexes are associated with human diseases. Furthermore,
chromosomal translocation of various cellular genes with those encoding HATs and
subunits of chromatin remodeling complexes have been implicated in leukomogenesis.
The *MOZ* (monocytic leukemia zinc finger) and *MLL/ALL-1* genes are frequently fused
to the gene encoding the co-activator HAT CBP [Sobulo *et al.*, *Proc. Natl. Acad. Sci.*
15 *USA* 94:8732-8737(1997)]. The resulting fusion protein MLL-CBP contains the
tandem bromodomain-PHD finger-HAT domain of CBP. It also has been shown that
both the bromodomain and HAT domain of CBP are required for leukomogenesis,
because deletion of either the bromodomain or the HAT domain results in loss of the
MLL-CBP fusion protein's ability for cell transform. These results indicate that the
20 CBP bromodomain, and more particularly, the ZA loop of the CBP bromodomain, is
an excellent target for developing drugs that interfere with the bromodomain acetyl-
lysine interaction that can be used in the treatment of human acute leukemia. In
addition, an antibody (*e.g.*, a humanized antibody) raised specifically against a peptide
from the ZA loop of the CBP bromodomain could also be effective for treating these
25 conditions.

Furthermore, the human immunodeficiency virus type 1 (HIV-1) *trans*-activator protein, Tat, is absolutely required for productive HIV viral replication [Jeang and Gagnol, *Curr. Top. Microbiol. Immunol.*, **188**:123-144(1994)]. Recently, it has been shown that HIV-1 Tat transcriptional activity is tightly regulated by lysine acetylation [Kiernan *et al.*, *EMBO Journal* **18**:6106-6118 (1999)]. Therefore, the interaction of the acetyl-lysine of Tat with one or more bromodomain-containing proteins associated

with chromatin remodeling could mediate gene transcription. Thus, the bromodomain/lysine-acetylated Tat interaction could also serve as a drug target for blocking HIV replication in cells. Similarly, an antibody raised specifically against a peptide from the ZA loop of the bromodomain could also be effective for treating these conditions.

In addition, based on the new structural information disclosed herein, the key amino acid residues for the binding of a given bromodomain and its binding partner can be identified and further elucidated using basic mutagenesis and standard isothermal titration calorimetry, for example. In this case, both the crucial amino acids for the bromodomain and the binding partner (i.e., apart from the acetyl-lysine) can be readily determined and are also part of the present invention.

The results obtained from the structural and functional studies disclosed herein provide the foundation for both high throughput drug screening and structure-based rational drug design. The agents identified by this procedure will be useful for ameliorating conditions involving chromatin remodeling/regulation as indicated above.

Structure based rational drug design is the most efficient method of drug development. However, heretofore, no information has been disclosed regarding the structure of the bromodomain or more importantly, its interaction with the acetyl-lysine of its binding partner. Obtaining detailed structural information requires an extensive NMR or X-ray crystallographic analysis. By determining and then exploiting the detailed structural information of the bromodomain and of the bromodomain/acetyl-histamine (exemplified by NMR analysis below) the present invention provides novel methods for developing new drugs through structure based rational drug design.

Thus the present invention provides representative sets of the atomic structure coordinates of the free form of the P/CAF bromodomain (Table 5) and of the P/CAF bromodomain-acetyl-histamine complex (Table 6) which were both obtained by NMR analysis. A Ribbon diagram of the three-dimensional structure of the P/CAF bromodomain is depicted in Figure 2E, whereas the P/CAF bromodomain acetyl-lysine

binding pocket is depicted in Figure 4. The present invention also provides the NOE-derived distance restraints, and NMR chemical shift assignments of the P/CAF bromodomain. The NMR chemical shift assignments of the P/CAF bromodomain are included in the chemical shift table (Table 1) for the ^1H - ^{15}N HSQC spectrum of P/CAF bromodomain. The unambiguous NOE-derived Inter-proton Distance Restraints (Table 2), the ambiguous NOE-derived Inter-proton Distance Restraints (Table 3) and the ^1H bonding restraints (Table 4) are also disclosed herein. The sample atomic coordinate data provided enable the skilled artisan to practice the invention. In addition, Tables 1-6 are also capable of being placed into a computer readable form which is also part of the present invention. Furthermore, methods of using these coordinates and chemical shifts and related information (including in computer readable forms) either individually or together in drug assays are also provided. More particularly, such atomic coordinates can be used to identify potential ligands or drugs which will modulate the binding of a bromodomain with its binding partner.

Therefore, if appearing herein, the following terms shall have the definitions set out below.

As used herein a “bromodomain-acetyl-lysine binding complex” is a binding complex between a bromodomain or fragment thereof and either a peptide/polypeptide comprising an acetyl-lysine (or an analog of acetyl-lysine), or a free analog of acetyl-lysine, such as acetyl-histamine disclosed in the Example below. Preferably, the peptide comprises at least six amino acids in addition to the acetyl-lysine. The dissociation constant of a bromodomain-acetyl-lysine binding complex is dependent on whether the lysine residue or analog thereof is acetylated or not, such that the affinity for the bromodomain and the peptide comprising the lysine residue (for example) significantly decreases when that lysine residue is not acetylated.

As used herein a “ZA loop” of a bromodomain is one portion of a bromodomain that is involved in the binding of the bromodomain to the acetyl-lysine. The structure of the ZA loop of the bromodomain of for P/CAF is depicted in Figure 2A. The ZA loop has between about 20 and 40 amino acids and comprises the amino acid sequence of SEQ ID NO:3. More preferably the ZA loop comprises between about 23 to 34 amino acids

and has the amino acid sequence SEQ ID NO:43. The amino acid sequence of the ZA loop for a representative number of individual bromodomains is shown in Figure 1.

A "polypeptide" or "peptide" comprising a fragment of a bromodomain, such as the
5 ZA loop, or a peptide or polypeptide comprising an acetyl-lysine, as used herein can be the "fragment" alone, or a larger chimeric or fusion peptide/protein which contains the "fragment".

As used herein the terms "fusion protein" and "fusion peptide" are used
10 interchangeably and encompass "chimeric proteins and/or chimeric peptides" and fusion "intein proteins/peptides". A fusion protein comprises at least a portion of a protein or peptide of the present invention, *e.g.*, a bromodomain, joined *via* a peptide bond to at least a portion of another protein or peptide including *e.g.*, a second bromodomain in a chimeric fusion protein. In a particular embodiment the portion of
15 the bromodomain is antigenic. Fusion proteins can comprise a marker protein or peptide, or a protein or peptide that aids in the isolation and/or purification of the protein, for example.

As used herein, and unless otherwise specified, the terms "agent", "potential drug",
20 "compound", "test compound" or "potential compound" are used interchangeably, and refer to chemicals which potentially have a use as an inhibitor or activator/stabilizer of bromodomain-acetyl-lysine binding. Therefore, such "agents", "potential drugs", "compounds" and "potential compounds" may be used, as described herein, in drug assays and drug screens and the like.

25 As used herein a "small organic molecule" is an organic compound, including a peptide [or organic compound complexed with an inorganic compound (*e.g.*, metal)] that has a molecular weight of less than 3 Kilodaltons. Such small organic molecules can be included as agents, etc. as defined above.

30 As used herein the term "binds to" is meant to include all such specific interactions that result in two or more molecules showing a preference for one another relative to some third molecule. This includes processes such as covalent, ionic, hydrophobic and

As used herein the term “about” signifies that a value is within twenty percent of the indicated value *i.e.*, a peptide containing "about" 20 amino acid residues can contain between 16 and 24 amino acid residues.

10 Partners of the Present Invention.

In accordance with the present invention there may be employed conventional molecular biology, microbiology, and recombinant DNA techniques within the skill of the art. Such techniques are explained fully in the literature. See, *e.g.*, Sambrook, Fritsch & Maniatis, *Molecular Cloning: A Laboratory Manual*, Second Edition (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (herein "Sambrook *et al.*, 1989"); *DNA Cloning: A Practical Approach*, Volumes I and II (D.N. Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed. 1984); *Nucleic Acid Hybridization* [B.D. Hames & S.J. Higgins eds. (1985)]; *Transcription And Translation* [B.D. Hames & S.J. Higgins, eds. (1984)]; *Animal Cell Culture* [R.I. Freshney, ed. (1986)]; *Immobilized Cells And Enzymes* [IRL Press, (1986)]; B. Perbal, *A Practical Guide To Molecular Cloning* (1984); F.M. Ausubel *et al.* (eds.), *Current Protocols in Molecular Biology*, John Wiley & Sons, Inc. (1994).

25 Therefore, if appearing herein, the following terms shall have the definitions set out below.

As used herein, the term "gene" refers to an assembly of nucleotides that encode a polypeptide, and includes cDNA and genomic DNA nucleic acids.

30

A "vector" is a replicon, such as plasmid, phage or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment. A "replicon" is any genetic element (e.g., plasmid, chromosome, virus) that functions

as an autonomous unit of DNA replication *in vivo*, *i.e.*, capable of replication under its own control.

A "cassette" refers to a segment of DNA that can be inserted into a vector at specific
 5 restriction sites. The segment of DNA encodes a polypeptide of interest, and the
 cassette and restriction sites are designed to ensure insertion of the cassette in the
 proper reading frame for transcription and translation.

A cell has been "transfected" by exogenous or heterologous DNA when such DNA has
 10 been introduced inside the cell.

A "nucleic acid molecule" refers to the phosphate ester polymeric form of
 ribonucleosides (adenosine, guanosine, uridine or cytidine; "RNA molecules") or
 deoxyribonucleosides (deoxyadenosine, deoxyguanosine, deoxythymidine, or
 15 deoxycytidine; "DNA molecules"), or any phosphoester analogues thereof, such as
 phosphorothioates and thioesters, in either single stranded form, or a double-stranded
 helix. Double stranded DNA-DNA, DNA-RNA and RNA-RNA helices are possible.
 The term nucleic acid molecule, and in particular DNA or RNA molecule, refers only
 to the primary and secondary structure of the molecule, and does not limit it to any
 20 particular tertiary forms. Thus, this term includes double-stranded DNA found, *inter*
alia, in linear or circular DNA molecules (*e.g.*, restriction fragments), plasmids, and
 chromosomes. In discussing the structure of particular double-stranded DNA
 molecules, sequences may be described herein according to the normal convention of
 giving only the sequence in the 5' to 3' direction along the nontranscribed strand of
 25 DNA (*i.e.*, the strand having a sequence homologous to the mRNA). A "recombinant
 DNA molecule" is a DNA molecule that has undergone a molecular biological
 manipulation.

A nucleic acid molecule is "hybridizable" to another nucleic acid molecule, such as a
 30 cDNA, genomic DNA, or RNA, when a single stranded form of the nucleic acid
 molecule can anneal to the other nucleic acid molecule under the appropriate
 conditions of temperature and solution ionic strength (*see* Sambrook *et al.*, *supra*).
 The conditions of temperature and ionic strength determine the "stringency" of the

hybridization. For preliminary screening for homologous nucleic acids, low stringency hybridization conditions, corresponding to a T_m of 55° , can be used, *e.g.*, 5x SSC, 0.1% SDS, 0.25% milk, and no formamide; or 30% formamide, 5x SSC, 0.5% SDS). Moderate stringency hybridization conditions correspond to a higher T_m , *e.g.*, 40% formamide, with 5x or 6x SCC. High stringency hybridization conditions correspond to the highest T_m , *e.g.*, 50% formamide, 5x or 6x SCC. Hybridization requires that the two nucleic acids contain complementary sequences, although depending on the stringency of the hybridization, mismatches between bases are possible. The appropriate stringency for hybridizing nucleic acids depends on the length of the nucleic acids and the degree of complementation, variables well known in the art. The greater the degree of similarity or homology between two nucleotide sequences, the greater the value of T_m for hybrids of nucleic acids having those sequences. The relative stability (corresponding to higher T_m) of nucleic acid hybridizations decreases in the following order: RNA:RNA, DNA:RNA, DNA:DNA. For hybrids of greater than 100 nucleotides in length, equations for calculating T_m have been derived (*see* Sambrook *et al.*, *supra*, 9.50-10.51). For hybridization with shorter nucleic acids, *i.e.*, oligonucleotides, the position of mismatches becomes more important, and the length of the oligonucleotide determines its specificity (*see* Sambrook *et al.*, *supra*, 11.7-11.8). Preferably a minimum length for a hybridizable nucleic acid is at least about 12 nucleotides; preferably at least about 18 nucleotides; and more preferably the length is at least about 27 nucleotides; and most preferably 36 nucleotides.

In a specific embodiment, the term "standard hybridization conditions" refers to a T_m of 55°C , and utilizes conditions as set forth above. In a preferred embodiment, the T_m is 60°C ; in a more preferred embodiment, the T_m is 65°C .

A DNA "coding sequence" is a double-stranded DNA sequence which is transcribed and translated into a polypeptide in a cell *in vitro* or *in vivo* when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxyl) terminus. A coding sequence can include, but is not limited to, prokaryotic sequences and synthetic DNA sequences. If the coding sequence is

intended for expression in a eukaryotic cell, a polyadenylation signal and transcription termination sequence will usually be located 3' to the coding sequence.

Transcriptional and translational control sequences are DNA regulatory sequences, such as promoters, enhancers, terminators, and the like, that provide for the expression of a coding sequence in a host cell. In eukaryotic cells, polyadenylation signals are control sequences.

A "promoter sequence" is a DNA regulatory region capable of binding RNA polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. For purposes of defining the present invention, the promoter sequence is bounded at its 3' terminus by the transcription initiation site and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter sequence will be found a transcription initiation site (conveniently defined for example, by mapping with nuclease S1), as well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase.

A coding sequence is "under the control" of transcriptional and translational control sequences in a cell when RNA polymerase transcribes the coding sequence into mRNA, which is then trans-RNA spliced and translated into the protein encoded by the coding sequence.

A DNA sequence is "operatively linked" to an expression control sequence when the expression control sequence controls and regulates the transcription and translation of that DNA sequence. The term "operatively linked" includes having an appropriate start signal (e.g., ATG) in front of the DNA sequence to be expressed and maintaining the correct reading frame to permit expression of the DNA sequence under the control of the expression control sequence and production of the desired product encoded by the DNA sequence. If a gene that one desires to insert into a recombinant DNA molecule does not contain an appropriate start signal, such a start signal can be inserted in front of the gene.

As used herein, the term "homologous" in all its grammatical forms refers to the relationship between proteins that possess a "common evolutionary origin," including proteins from superfamilies (*e.g.*, the immunoglobulin superfamily) and homologous proteins from different species (*e.g.*, myosin light chain, etc.) [Reeck *et al.*, *Cell*, 5 50:667 (1987)]. Such proteins have sequence homology as reflected by their high degree of sequence similarity.

Accordingly, the term "sequence similarity" in all its grammatical forms refers to the degree of identity or correspondence between nucleic acid or amino acid sequences of 10 proteins that may or may not share a common evolutionary origin (*see* Reeck *et al.*, *supra*). However, in common usage and in the instant application, the term "homologous," when modified with an adverb such as "highly," may refer to sequence similarity and not a common evolutionary origin.

15 Two DNA sequences are "substantially homologous" when at least about 60% (preferably at least about 80%, and most preferably at least about 90 or 95%) of the nucleotides match over the defined length of the DNA sequences. Sequences that are substantially homologous can be identified by comparing the sequences using standard software available in sequence data banks, or in a Southern hybridization experiment 20 under, for example, stringent conditions as defined for that particular system. Defining appropriate hybridization conditions is within the skill of the art. See, *e.g.*, Maniatis *et al.*, *supra*; DNA Cloning, Vols. I & II, *supra*; Nucleic Acid Hybridization, *supra*.

As used herein an amino acid sequence is 100% "homologous" to a second amino acid 25 sequence if the two amino acid sequences are identical, and/or differ only by neutral or conservative substitutions as defined below. Accordingly, an amino acid sequence is 50% "homologous" to a second amino acid sequence if 50% of the two amino acid sequences are identical, and/or differ only by neutral or conservative substitutions.

30 As used herein, DNA and protein sequence percent identity can be determined using MacVector 6.0.1, Oxford Molecular Group PLC (1996) and the Clustal W algorithm with the alignment default parameters, and default parameters for identity. These

002220"4FE0T560

commercially available programs can also be used to determine sequence similarity using the same or analogous default parameters.

The term "corresponding to" is used herein to refer similar or homologous sequences, whether the exact position is identical or different from the molecule to which the similarity or homology is measured. Thus, the term "corresponding to" refers to the sequence similarity, and not the numbering of the amino acid residues or nucleotide bases.

As used herein a "heterologous nucleotide sequence" is a nucleotide sequence that is added to a nucleotide sequence of the present invention by recombinant methods to form a nucleic acid which is not naturally formed in nature. Such nucleic acids can encode fusion proteins or peptides, including chimeric proteins and peptides. Thus the heterologous nucleotide sequence can encode peptides and/or proteins which contain regulatory and/or structural properties. In another such embodiment the heterologous nucleotide can encode a protein or peptide that functions as a means of detecting the protein or peptide encoded by the nucleotide sequence of the present invention after the recombinant nucleic acid is expressed. In still another such embodiment the heterologous nucleotide can function as a means of detecting a nucleotide sequence of the present invention. A heterologous nucleotide sequence can comprise non-coding sequences including restriction sites, regulatory sites, promoters and the like.

The present invention also relates to cloning vectors containing nucleic acids encoding analogs and derivatives of the bromodomains of the present invention and polypeptides/peptides that can bind a bromodomain when a lysine of the polypeptide/peptide is acetylated, including modified fragments, that have the same or homologous functional activity as the individual fragments, and homologs thereof. The production and use of derivatives and analogs related to the fragments are within the scope of the present invention.

Due to the degeneracy of nucleotide coding sequences, other DNA sequences which encode substantially the same amino acid sequence as a nucleic acid encoding a protein

comprising bromodomain or bromodomain binding partner (*i.e.*, when post-transcriptionally acetylated) of the present invention for example, may be used in the practice of the present invention. These include but are not limited to allelic genes, homologous genes from other species, which are altered by the substitution of different

5 codons that encode the same amino acid residue within the sequence, thus producing a silent change. Likewise, the peptides and polypeptides of the present invention include, but are not limited to, those containing, as a primary amino acid sequence, analogous portions of their respective amino acid sequences including altered sequences in which functionally equivalent amino acid residues are substituted for

10 residues within the sequence resulting in a conservative amino acid substitution. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of a similar polarity, which acts as a functional equivalent, resulting in a silent alteration. Substitutes for an amino acid within the sequence may be selected from other members of the class to which the amino acid belongs. For

15 example, the nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine. Amino acids containing aromatic ring structures are phenylalanine, tryptophan, and tyrosine. The polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine. The positively charged (basic) amino acids include arginine, and lysine.

20 The negatively charged (acidic) amino acids include aspartic acid and glutamic acid.

Particularly preferred conserved amino acid exchanges are:

- (a) Lys for Arg or vice versa such that a positive charge may be maintained;
- (b) Glu for Asp or vice versa such that a negative charge may be maintained;
- 25 (c) Ser for Thr or vice versa such that a free -OH can be maintained;
- (d) Gln for Asn or vice versa such that a free NH₂ can be maintained;
- (e) Ile for Leu or for Val or vice versa as roughly equivalent hydrophobic amino acids; and
- (f) Phe for Tyr or vice versa as roughly equivalent aromatic amino acids.

30

A conservative change generally leads to less change in the structure and function of the resulting protein. A non-conservative change is more likely to alter the structure,

activity or function of the resulting protein. The present invention should be considered to include sequences containing conservative changes which do not significantly alter the activity or binding characteristics of the resulting protein.

Specific amino acid residues for the P/CAF bromodomain have been identified that are important for binding, indicating a potential lower stringency for the substitution of the remaining amino acids residues.

All of the peptides/fragments of the present invention can be modified by being placed in a fusion or chimeric peptide or protein, or labeled *e.g.*, to have an N-terminal FLAG-tag, or H6 tag. In a particular embodiment the P/CAF bromodomain fragment can be modified to contain a marker protein such as green fluorescent protein as described in U.S. Patent No. 5,625,048 filed April 29, 1997 and WO 97/26333, published July 24, 1997 each of which are hereby incorporated by reference herein in their entireties.

The nucleic acids encoding peptides and protein fragments of the present invention and analogs thereof can be produced by various methods known in the art. The manipulations which result in their production can occur at the gene or protein level [Sambrook *et al.*, 1989, *supra*]. The nucleotide sequence can be cleaved at appropriate sites with restriction endonuclease(s), followed by further enzymatic modification if desired, isolated, and ligated *in vitro*. In addition a nucleic acid sequence can be mutated *in vitro* or *in vivo*, to create and/or destroy translation, initiation, and/or termination sequences, or to create variations in coding regions and/or form new restriction endonuclease sites or destroy preexisting ones, to facilitate further *in vitro* modification. Any technique for mutagenesis known in the art can be used, including but not limited to, *in vitro* site-directed mutagenesis [Hutchinson *et al.*, *J. Biol. Chem.*, **253**:6551 (1978); Zoller and Smith, *DNA*, **3**:479-488 (1984); Oliphant *et al.*, *Gene*, **44**:177 (1986); Hutchinson *et al.*, *Proc. Natl. Acad. Sci. U.S.A.*, **83**:710 (1986)], use of TAB® linkers (Pharmacia), etc. PCR techniques are preferred for site directed mutagenesis [see Higuchi, 1989, "Using PCR to Engineer DNA", in *PCR Technology: Principles and Applications for DNA Amplification*, H. Erlich, ed., Stockton Press, Chapter 6, pp. 61-70].

5

A bacterial protein expression system can be used to make various stable isotopically labeled (^{13}C , ^{15}N , and ^2H) protein samples that are useful for a three-dimensional NMR structural determination of a protein complex. For example a pET14b (Novagen) bacterial expression vector can be constructed which expresses the recombinant P/CAF
10 bromodomain as an amino-terminal His-tagged fusion protein.

Protein expression and purification can be conducted using standard procedures for His-tagged proteins [Zhou *et al.*, *J. Biol. Chem.* **270**:31119-31123 (1995)]. To optimize the level of protein expression, various bacterial growth and expression conditions can be screened, which include different *E. Coli* cell lines, and growth and protein induction temperatures. Generally, it is preferred to obtain the maximum amount of soluble protein while still inducing protein expression with a relatively low IPTG concentration *e.g.*, ~0.2mM (final concentration) at 16°C. As exemplified below, the bromodomain of P/CAF (residues 719-832 of SEQ ID NO:2 which is SEQ ID NO:7) was subcloned into the pET14b expression vector (Novagen) and expressed in *Escherichia coli* BL21(DE3) cells. Uniformly ¹⁵N- and ¹⁵N/¹³C-labeled proteins were prepared by growing bacteria in a minimal medium containing ¹⁵NH₄Cl with or without ¹³C₆-glucose. A uniformly ¹⁵N/¹³C-labeled and fractionally deuterated protein sample was prepared by growing the cells in 75% ²H₂O. The bromodomain was purified by affinity chromatography on a nickel-IDA column (Invitrogen) followed by the removal of poly-His tag by thrombin cleavage. The final purification of the protein was achieved by size-exclusion chromatography. The acetyl-lysine-containing peptides were prepared on a MilliGen 9050 peptide synthesizer (Perkin Elmer) using Fmoc/HBTU chemistry. Acetyl-lysine was incorporated using the reagent Fmoc-Ac-Lys with HBTU/DIPEA activation. NMR samples contained approximately 1 mM protein in 100mM phosphate buffer of pH 6.5 and 5mM perdeuterated DTT and 0.5mM EDTA in H₂O/²H₂O (9/1) or ²H₂O.

One major advantage of using the heteronuclear multidimensional approach, as exemplified herein, is that the NMR resonance assignments of a protein are obtained in a sequence-specific manner which assures accuracy and greatly facilitates data analysis and structure determination [Clare, G. M. & Gronenborn, A. M. *Meth. Enzymol.*

- 5 **239:249-363 (1994)**]. In addition, the signal overlapping problems in the protein spectra are minimized by the use of multidimensional NMR spectra, which separates the proton signals according to the chemical shifts of their attached hetero-nuclei (such as ^{15}N and ^{13}C). This NMR approach has been proven very powerful for structural analysis of large proteins [Clare, G. M. & Gronenborn, A. M. *Meth. Enzymol.*
- 10 **239:249-363 (1994)**]. To facilitate sequence-specific resonance assignments for the structural study, a uniformly ^{13}C , ^{15}N -labeled and fractionally (75%) deuterated protein sample of the bromodomain can be prepared by growing bacterial cells in 75% $^2\text{H}_2\text{O}$ as exemplified below. Such protein samples can be used for triple-resonance NMR experiments. A triple-labeled protein sample is useful for high-resolution NMR
- 15 structural studies. Because of the favorable ^1H , ^{13}C , and ^{15}N relaxation rates caused by the partial deuteration of the protein, constant-time triple-resonance NMR spectra can be acquired with higher digital resolution and sensitivity [Sattler, M. & Fesik, S. W. *Structure* **4:1245-1249 (1996)**]. In addition, various stable-isotopically labeled (^{15}N and ^{13}C / ^{15}N) proteins can also be prepared using this procedure.

20

Synthetic Polypeptides

- The term "polypeptide" is used in its broadest sense to refer to a compound of two or more subunit amino acids, amino acid analogs, or peptidomimetics. The subunits are
- 25 linked by peptide bonds. The terms "polypeptide", "protein", and "peptide" are used interchangeably herein, though preferably as used herein a "peptide" refers to a compound of at least two but less than fifty subunit amino acids, and a polypeptide or protein refers to compound of fifty or more amino acids. The polypeptides of the present invention may be chemically synthesized or as detailed above, genetically
- 30 engineered or isolated from natural sources.

In addition, potential drugs or agents that may be tested in the drug screening assays of the present invention may also be chemically synthesized. When the peptide is to be

modified, *e.g.*, acetylated, the modification can be at any time during the peptide synthesis, including using an acetyl-lysine as a starting material or acetylating a lysine residue of a peptide after the peptide has been synthesized. In the Example below, the acetyl-lysine-containing peptides were prepared on a MilliGen 9050 peptide synthesizer (Perkin Elmer) using Fmoc/HBTU chemistry. Acetyl-lysine was incorporated using the reagent Fmoc-Ac-Lys with HBTU/DIPEA activation.

Thus, synthetic polypeptides, prepared using the well known techniques of solid phase, liquid phase, or peptide condensation techniques, or any combination thereof, can include natural and unnatural amino acids. Amino acids used for peptide synthesis may be standard Boc (N^{α} -amino protected N^{α} -t-butyloxycarbonyl) amino acid resin with the standard deprotecting, neutralization, coupling and wash protocols of the original solid phase procedure of Merrifield [*J. Am. Chem. Soc.*, **85**:2149-2154 (1963)], or the base-labile N^{α} -amino protected 9-fluorenylmethoxycarbonyl (Fmoc) amino acids first described by Carpino and Han [*J. Org. Chem.*, **37**:3403-3409 (1972)]. Both Fmoc and Boc N^{α} -amino protected amino acids can be obtained from Fluka, Bachem, Advanced Chemtech, Sigma, Cambridge Research Biochemical, Bachem, or Peninsula Labs or other chemical companies familiar to those who practice this art. In addition, the method of the invention can be used with other N^{α} -protecting groups that are familiar to those skilled in this art. Solid phase peptide synthesis may be accomplished by techniques familiar to those in the art and provided, for example, in Stewart and Young [Solid Phase Synthesis, Second Edition, Pierce Chemical Co., Rockford, IL (1984)] and Fields and Noble [*Int. J. Pept. Protein Res.*, **35**:161-214 (1990)], or using automated synthesizers, such as sold by ABS. Thus, polypeptides of the invention may comprise D-amino acids, a combination of D- and L-amino acids, and various "designer" amino acids (*e.g.*, β -methyl amino acids, $C\alpha$ -methyl amino acids, and $N\alpha$ -methyl amino acids, etc.) to convey special properties. Synthetic amino acids include ornithine for lysine, fluorophenylalanine for phenylalanine, and norleucine for leucine or isoleucine. Additionally, by assigning specific amino acids at specific coupling steps, α -helices, β turns, β sheets, γ -turns, and cyclic peptides can be generated.

In a further embodiment, subunits of peptides that confer useful chemical and structural properties will be chosen. For example, peptides comprising D-amino acids will be resistant to L-amino acid-specific proteases *in vivo*. In addition, the present invention envisions preparing peptides that have more well defined structural

5 properties, and the use of peptidomimetics, and peptidomimetic bonds, such as ester bonds, to prepare peptides with novel properties. In another embodiment, a peptide may be generated that incorporates a reduced peptide bond, i.e., $R_1\text{-CH}_2\text{-NH-R}_2$, where R_1 and R_2 are amino acid residues or sequences. A reduced peptide bond may be introduced as a dipeptide subunit. Such a molecule would be resistant to peptide bond

10 hydrolysis, *e.g.*, protease activity. Such peptides would provide ligands with unique function and activity, such as extended half-lives *in vivo* due to resistance to metabolic breakdown, or protease activity. Furthermore, it is well known that in certain systems constrained peptides show enhanced functional activity [Hruby, *Life Sciences*, **31**:189-199 (1982); Hruby *et al.*, *Biochem J.*, **268**:249-262 (1990)]; the present invention

15 provides a method to produce a constrained peptide that incorporates random sequences at all other positions.

Constrained and cyclic peptides. A constrained, cyclic or rigidized peptide may be prepared synthetically, provided that in at least two positions in the sequence of the

20 peptide an amino acid or amino acid analog is inserted that provides a chemical functional group capable of crosslinking to constrain, cyclise or rigidize the peptide after treatment to form the crosslink. Cyclization will be favored when a turn-inducing amino acid is incorporated. Examples of amino acids capable of crosslinking a peptide are cysteine to form disulfides, aspartic acid to form a lactone or a lactam, and a

25 chelator such as γ -carboxyl-glutamic acid (Gla) (Bachem) to chelate a transition metal and form a cross-link. Protected γ -carboxyl glutamic acid may be prepared by modifying the synthesis described by Zee-Cheng and Olson [*Biophys. Biochem. Res. Commun.*, **94**:1128-1132 (1980)]. A peptide in which the peptide sequence comprises at least two amino acids capable of crosslinking may be treated, *e.g.*, by oxidation of

30 cysteine residues to form a disulfide or addition of a metal ion to form a chelate, so as to crosslink the peptide and form a constrained, cyclic or rigidized peptide.

The present invention provides strategies to systematically prepare cross-links. For example, if four cysteine residues are incorporated in the peptide sequence, different protecting groups may be used (Hiskey, in *The Peptides: Analysis, Synthesis, Biology*, Vol. 3, Gross and Meienhofer, eds., Academic Press: New York, pp. 137-167 (1981); Ponsanti *et al.*, *Tetrahedron*, **46**:8255-8266 (1990)]. The first pair of cysteines may be deprotected and oxidized, then the second set may be deprotected and oxidized. In this way a defined set of disulfide cross-links may be formed. Alternatively, a pair of cysteines and a pair of chelating amino acid analogs may be incorporated so that the cross-links are of a different chemical nature.

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Non-classical amino acids that induce conformational constraints. The following non-classical amino acids may be incorporated in the peptide in order to introduce particular conformational motifs: 1,2,3,4-tetrahydroisoquinoline-3-carboxylate [Kazmierski *et al.*, *J. Am. Chem. Soc.*, **113**:2275-2283 (1991)]; (2S,3S)-methyl-phenylalanine, (2S,3R)-methyl-phenylalanine, (2R,3S)-methyl-phenylalanine and (2R,3R)-methyl-phenylalanine (Kazmierski and Hruby, *Tetrahedron Lett.* (1991)]; 2-aminotetrahydronaphthalene-2-carboxylic acid [Landis, Ph.D. Thesis, University of Arizona (1989)]; hydroxy-1,2,3,4-tetrahydroisoquinoline-3-carboxylate [Miyake *et al.*, *J. Takeda Res. Labs.*, **43**:53-76 (1989)]; β -carboline (D and L) [Kazmierski, Ph.D. Thesis, University of Arizona (1988)]; HIC (histidine isoquinoline carboxylic acid) [Zechel *et al.*, *Int. J. Pep. Protein Res.*, **43** (1991)]; and HIC (histidine cyclic urea) (Dharanipragada).

The following amino acid analogs and peptidomimetics may be incorporated into a peptide to induce or favor specific secondary structures: LL-Acp (LL-3-amino-2-propenidone-6-carboxylic acid), a β -turn inducing dipeptide analog [Kemp *et al.*, *J. Org. Chem.*, **50**:5834-5838 (1985)]; β -sheet inducing analogs [Kemp *et al.*, *Tetrahedron Lett.*, **29**:5081-5082 (1988)]; β -turn inducing analogs [Kemp *et al.*, *Tetrahedron Lett.*, **29**:5057-5060 (1988)]; α -helix inducing analogs (Kemp *et al.*, *Tetrahedron Lett.*, **29**:4935-4938 (1988)]; γ -turn inducing analogs [Kemp *et al.*, *J. Org. Chem.*, **54**:109:115 (1989)]; and analogs provided by the following references: Nagai and Sato, *Tetrahedron Lett.*, **26**:647-650 (1985); DiMaio *et al.*, *J. Chem. Soc. Perkin Trans.*, p. 1687 (1989); also a Gly-Ala turn analog [Kahn *et al.*, *Tetrahedron*

Lett., **30**:2317 (1989)]; amide bond isostere [Jones *et al.*, *Tetrahedron Lett.*, **29**:3853-3856 (1988)]; tretrazol [Zabrocki *et al.*, *J. Am. Chem. Soc.*, **110**:5875-5880 (1988)]; DTC [Samanen *et al.*, *Int. J. Protein Pep. Res.*, **35**:501:509 (1990)]; and analogs taught in Olson *et al.*, *J. Am. Chem. Sci.*, **112**:323-333 (1990) and Garvey *et al.*, *J. Org. Chem.*, **56**:436 (1990). Conformationally restricted mimetics of beta turns and beta bulges, and peptides containing them, are described in U.S. Patent No. 5,440,013, issued August 8, 1995 to Kahn.

Structure-based Mutation Analysis

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Protein structural analysis using NMR spectroscopy has several unique advantages. In addition to high-resolution three-dimensional structural information, the chemical shift assignments for the protein obtained in the structural study further provides a map of the entire protein at the atomic level, which can be used for structure-based

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biochemical analysis of protein-protein interactions. For example, the information generated from the NMR structural analysis can also serve to identify specific amino acid residues in the peptide-binding site for complementary mutagenesis studies.

Specific focus can be placed on those residues that display long-range NOEs (particularly the side-chain NOEs in the ^{13}C -NOESY data) between the bromodomain

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and a peptide comprising an acetyl-lysine.

To ensure mutant proteins are valid for functional analysis, it can be determined as to whether a mutation results in any significant perturbation of the overall conformation of the bromodomain, particularly the effects of mutation on the acetyl-lysine binding sites. NMR spectroscopy is a powerful method for examining the effects of such a mutation on the conformation of the protein. One can readily obtain information about the global conformation of a mutant protein from the proton (^1H) 1D spectrum, by examining the chemical shift dispersion and peak line-width of NMR signals of amide, aromatic and aliphatic protons. Moreover, 2D ^1H - ^{15}N HSQC spectra reveal details of the effects of a mutation on both local and global conformation of the protein, since every single $^1\text{H}/^{15}\text{N}$ signal (both the chemical shift and line-shape) in the NMR spectrum is a "reporter" for a particular amino acid residue. Thus, to assess how mutations effect protein stability and the overall protein conformation, the ^{15}N HSQC

spectra of mutated proteins can be compared to that of the wild-type protein bromodomain.

Chemical-shift perturbations due to ligand binding have proven to be a reliable and sensitive probe for the ligand binding site of the protein. This is because the chemical-shift changes of the backbone amide groups are likely to reflect any changes in protein conformation and/or hydrogen bonding due to the peptide/ligand binding. To examine the effects of a mutation on the ligand binding (in this case the ligand is a peptide comprising an acetyl-lysine), peptide titration experiments can be conducted by following the changes of $^1\text{H}/^{15}\text{N}$ signals of the mutant proteins as a function of the peptide concentration. These experiments indicate whether the acetyl-lysine binding site remains the same or changes in the mutants relative to the wild type protein. The effects of the mutation on the peptide binding affinity can also be examined by NMR spectroscopy. If the mutated proteins result in the reduction of the binding affinity, a change of the exchange phenomenon between the free and the ligand-bound signals should be observed in NMR spectrum. If the reduction in binding affinity causes the peptide binding to change from a slow exchange rate to a fast exchange rate, on the NMR time scale, then the peptide binding affinity can be determined from the NMR titration experiment. From these mutation analyses key amino acid residues that are important for binding a peptide comprising the acetyl-lysine can be identified. Such analysis has been exemplified below.

Protein Structure Determination by NMR Spectroscopy

The NMR results from the present invention are summarized by the atomic structure coordinates of the free form of the P/CAF bromodomain (Table 5) and of the P/CAF bromodomain-acetyl-histamine complex (Table 6). The NMR chemical shift assignments of the P/CAF bromodomain are included in the chemical shift table (Table 1) for the ^1H - ^{15}N HSQC spectrum of P/CAF bromodomain. The unambiguous NOE-derived Inter-proton Distance Restraints are in Table 2, the ambiguous NOE-derived Inter-proton Distance Restraints are in Table 3, and the ^1H bonding restraints are disclosed in Table 4.

Backbone and Side-chain Assignments: Sequence-specific backbone assignment can be achieved by using a suite of deuterium-decoupled triple-resonance 3D NMR experiments which include HNCA, HN(CO)CA, HN(CA)CB, HN(COCA)CB, HNCO, and HN(CA)CO experiments [Yamazaki, *et al.*, *J. Am. Chem. Soc.* **116**:11655-11666 (1994)]. The water flip-back scheme is used in these NMR pulse programs to minimize amide signal attenuation from water exchange. Sequential side-chain assignments are typically accomplished from a series of 3D NMR experiments with alternative approaches to confirm the assignments. These experiments include 3D ^{15}N TOCSY-HSQC, HCCH-TOCSY, (H)C(CO)NH-TOCSY, and H(C)(CO)NH-TOCSY [see Clore, G. M. & Gronenborn, A. M. *Meth. Enzymol.* **239**:249-363 (1994); Sattler *et al.*, *Prog. in Nuclear Magnetic Resonance Spec.* **4**:93-158 (1999)].

Stereospecific Methyl Groups: Stereospecific assignments of methyl groups of Valine and Leucine residues can be obtained from an analysis of carbon signal multiplet splitting using a fractionally ^{13}C -labeled protein sample, which can be readily prepared using M9 minimal medium containing 10% ^{13}C -/90% ^{12}C -glucose mixture [see Neri, *et al.*, *Biochemistry* **28**:7510-7516 (1989)].

Dihedral Angle Restraints: Backbone dihedral angle (Φ) constraints can be generated from the $^3J_{\text{HNH}\alpha}$ coupling constants measured in a HNHA-*J* experiment [see Vuister, G. & Bax, A. *J. Am. Chem. Soc.* **115**:7772-7777 (1993)]. Side-chain dihedral angles (χ_1) can be obtained from short mixing time ^{15}N -edited 3D TOCSY-HSQC [see Clore, *et al.*, *J. Biomol. NMR* **1**:13-22 (1991)] and 3D HNHB experiments [see Matson *et al.*, *J. Biomol. NMR* **3**:239-244 (1993)], which can also provide stereospecific assignments of β methylene protons.

Hydrogen Bonds Restraints: Amide protons that are involved in hydrogen bonds can be identified from an analysis of amide exchange rates measured from a series of 2D $^1\text{H}/^{15}\text{N}$ HSQC spectra recorded after adding $^2\text{H}_2\text{O}$ to the protein sample.

NOE Distance Restraints: Distance restraints are obtained from analysis of ^{15}N , and ^{13}C -edited 3D NOESY data, which can be collected with different mixing times to minimize spin diffusion problems. The nuclear Overhauser effect (NOE)-derived

restraints are categorized as strong (1.8-3 Å), medium (1.8-4 Å) or weak (1.8-5 Å) based on the observed NOE intensities. A recently developed procedure for the iterative automated NOE analysis by using ARIA [see Nilges *et al.*, *Prog. NMR Spectroscopy* **32**:107-139 (1998)] can be employed which integrates with X-PLOR for structural calculations. To ensure the success of ARIA/X-PLOR-assisted NOE analysis and structure calculations, the ARIA assigned NOE peaks can be manually confirmed.

Intermolecular NOE Distance Restraints: For the structural determination of a protein/peptide complex, intermolecular NOE distance restraints can be obtained from a ^{13}C -edited (F_1) and ^{15}N , and ^{13}C -filtered (F_3) 3D NOESY data set collected for a sample containing isotope-labeled protein and non-labeled peptide.

Structure Calculations and Refinements: Structures of the protein can be generated using a distance geometry/simulated annealing protocol with the X-PLOR program [see Nilges, *et al.*, *FEBS Lett.* **229**:317-324 (1988); Kuszewski, *et al.*, *J. Biomol. NMR* **2**:33-56 (1992); Brünger, A. T. *X-PLOR Version 3.1: A system for X-Ray crystallography and NMR* (Yale University Press, New Haven, CT, 1993)]. The structure calculations can employ inter-proton distance restraints obtained from ^{15}N - and ^{13}C -resolved NOESY spectra. The initial low-resolution structures can be used to facilitate NOE assignments, and help identify hydrogen bonding partners for slowly exchanging amide protons. The experimental restraints of dihedral angles and hydrogen bonds can be included in the distance restraints for structure refinements.

Protein-Structure Based Design of Agonists and Antagonists of the Bromodomain-Acetyl-Lysine Binding Complex

Once the three-dimensional structure of the Bromodomain and the Bromodomain-acetyl-lysine binding complex are determined, a potential drug or agent (antagonist or agonist) can be examined through the use of computer modeling using a docking program such as GRAM, DOCK, or AUTODOCK [Dunbrack *et al.*, 1997, *supra*]. This procedure can include computer fitting of potential agents to the bromodomain, for example, to ascertain how well the shape and the chemical structure of the potential ligand will complement or interfere with the interaction between the bromodomain and

the acetyl-lysine [Bugg *et al.*, *Scientific American*, **Dec.**:92-98 (1993); West *et al.*, *TIPS*, **16**:67-74 (1995)]. Computer programs can also be employed to estimate the attraction, repulsion, and steric hindrance of the agent to the dimer-dimer binding site, for example. Generally the tighter the fit (*e.g.*, the lower the steric hindrance, and/or the greater the attractive force) the more potent the potential drug will be since these properties are consistent with a tighter binding constant. Furthermore, the more specificity in the design of a potential drug the more likely that the drug will not interfere with related proteins. This will minimize potential side-effects due to unwanted interactions with other proteins.

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Initially a potential drug could be obtained by screening a random peptide library produced by recombinant bacteriophage for example, [Scott and Smith, *Science*, **249**:386-390 (1990); Cwirla *et al.*, *Proc. Natl. Acad. Sci.*, **87**:6378-6382 (1990); Devlin *et al.*, *Science*, **249**:404-406 (1990)] or a chemical library. An agent selected in this manner could be then be systematically modified by computer modeling programs until one or more promising potential drugs are identified. Such analysis has been shown to be effective in the development of HIV protease inhibitors [Lam *et al.*, *Science* **263**:380-384 (1994); Wlodawer *et al.*, *Ann. Rev. Biochem.* **62**:543-585 (1993); Appelt, *Perspectives in Drug Discovery and Design* **1**:23-48 (1993); Erickson, *Perspectives in Drug Discovery and Design* **1**:109-128 (1993)].

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Such computer modeling allows the selection of a finite number of rational chemical modifications, as opposed to the countless number of essentially random chemical modifications that could be made, any one of which might lead to a useful drug. Each chemical modification requires additional chemical steps, which while being reasonable for the synthesis of a finite number of compounds, quickly becomes overwhelming if all possible modifications needed to be synthesized. Thus, through the use of the three-dimensional structural analysis disclosed herein and computer modeling, a large number of these compounds can be rapidly screened on the computer monitor screen, and a few likely candidates can be determined without the laborious synthesis of untold numbers of compounds.

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Phage libraries have been constructed which when infected into host *E. coli* produce random peptide sequences of approximately 10 to 15 amino acids [Parmley and Smith,

Gene 73:305-318 (1988), Scott and Smith, Science 249:386-249 (1990)]. Specifically, the phage library can be mixed in low dilutions with permissive *E. coli* in low melting point LB agar which is then poured on top of LB agar plates. After incubating the plates at 37°C for a period of time, small clear plaques in a lawn of *E. coli* will form which represents active phage growth and lysis of the *E. coli*. A representative of these phages can be absorbed to nylon filters by placing dry filters onto the agar plates. The filters can be marked for orientation, removed, and placed in washing solutions to block any remaining absorbent sites. The filters can then be placed in a solution containing, for example, a radioactive bromodomain. After a specified incubation period, the filters can be thoroughly washed and developed for autoradiography. Plaques containing the phage that bind to the radioactive bromodomain can then be identified. These phages can be further cloned and then retested for their ability to bind to the bromodomain as before. Once the phage has been purified, the binding sequence contained within the phage can be determined by standard DNA sequencing techniques. Once the DNA sequence is known, synthetic peptides can be generated which are encoded by these sequences. These peptides can be tested, for example, for their ability to modulate the affinity of the bromodomain for its binding partner (*e.g.*, a protein comprising an acetyl-lysine or a fragment of that protein).

The effective peptide(s) can be synthesized in large quantities for use in *in vivo* models and eventually in humans to treat certain tumors. It should be emphasized that synthetic peptide production is relatively non-labor intensive, easily manufactured, quality controlled and thus, large quantities of the desired product can be produced quite cheaply. Similar combinations of mass produced synthetic peptides have been used with great success [Patarroyo, *Vaccine*, 10:175-178 (1990)].

Drug Screening Assays

The drug screening assays of the present invention may use any of a number of means for determining the interaction between an agent or drug and a peptide comprising an acetyl-lysine and/or a bromodomain. Thus, standard high throughput drug screening procedures can be employed using a library of low molecular weight compounds, for

example that can be screened to identify a binding partner for the bromodomain. Any such chemical library can be used including those discussed above.

In a particular assay, a bromodomain is placed on or coated onto a solid support.

- 5 Methods for placing the peptides or proteins on the solid support are well known in the art and include such things as linking biotin to the protein and linking avidin to the solid support. An agent is allowed to equilibrate with the bromodomain to test for binding. Generally, the solid support is washed and agents that are retained are selected as potential drugs. Alternatively, a peptide comprising an acetyl-lysine is
- 10 placed on or coated onto a solid support. In a particular embodiment of this type, the peptide comprises the amino acid sequence of SEQ ID NO:4.

- The agent may be labeled. For example, in one embodiment radiolabeled agents are used to measure the binding of the agent. In another embodiment the agents have
- 15 fluorescent markers. In yet another embodiment, a Biocore chip (Pharmacia) coated with the bromodomain is used, for example and the change in surface conductivity can be measured.

- In addition, since a number of proteins have been identified that contain
- 20 bromodomains, and the binding partners of many of these proteins are known, the fact that the bromodomain specifically binds to an acetylated lysine as disclosed herein allows the identification and preparation of a number of potential modulators of the bromodomain-acetyl-lysine binding complex based on the amino acid sequences of the binding partners to the proteins. Such potential modulators include : ISYGR-AcK-
- 25 KRRQRR (SEQ ID NO:4), ARKSTGG-AcK-APRKQL (SEQ ID NO:5) and QSTSRHK-AcK-LMFKTE (SEQ ID NO:6) which bind to the P/CAF bromodomain as shown in the Example, below. Such peptides also can be used, for example, as a starting point for the design of an inhibitor of the bromodomain-acetyl-lysine binding complex.

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Alternatively, a drug can be specifically designed to bind to the ZA loop of a bromodomain for example, such as the P/CAF bromodomain, and be assayed through NMR based methodology [Shuker *et al.*, *Science* 274:1531-1534 (1996) hereby

incorporated by reference in its entirety.] In a particular embodiment, analogs of the binding partner of the bromodomain can be used in this analysis. One such peptide has the amino acid sequence of SEQ ID NO:4. In another embodiment of this type, the peptide has the amino acid sequence of SEQ ID NO:5. In another such embodiment of
 5 this type, the peptide has the amino acid sequence of SEQ ID NO:6.

The assay begins with contacting a compound with a ^{15}N -labeled bromodomain. Binding of the compound with the ZA loop of the bromodomain can be determined by monitoring the ^{15}N - or ^1H -amide chemical shift changes in two dimensional ^{15}N -
 10 heteronuclear single-quantum correlation (^{15}N -HSQC) spectra upon the addition of the compound to the ^{15}N -labeled bromodomain. Since these spectra can be rapidly obtained, it is feasible to screen a large number of compounds [Shuker *et al.*, *Science* **274**:1531-1534 (1996)]. A compound is identified as a potential ligand if it binds to the ZA loop of the bromodomain. In a further embodiment, the potential ligand can
 15 then be used as a model structure, and analogs to the compound can be obtained (e.g, from the vast chemical libraries commercially available, or alternatively through *de novo* synthesis). The analogs are then screened for their ability to bind the ZA loop of the bromodomain thus to obtain a ligand. An analog of the potential ligand is chosen as a ligand when it binds to the ZA loop of the bromodomain with a higher binding
 20 affinity than the potential ligand. In a preferred embodiment of this type the analogs are screened by monitoring the ^{15}N - or ^1H -amide chemical shift changes in two dimensional ^{15}N -heteronuclear single-quantum correlation (^{15}N -HSQC) spectra upon the addition of the analog to the ^{15}N -labeled bromodomain as described above.

25 In another further embodiment, compounds are screened for binding to two nearby sites on the bromodomain. In this case, a compound that binds a first site of the bromodomain does not bind a second nearby site. Binding to the second site can be determined by monitoring changes in a different set of amide chemical shifts in either the original screen or a second screen conducted in the presence of a ligand (or
 30 potential ligand) for the first site. From an analysis of the chemical shift changes the approximate location of a potential ligand for the second site is identified. Optimization of the second ligand for binding to the site is then carried out by screening structurally related compounds (e.g., analogs as described above). When

- ligands for the first site and the second site are identified, their location and orientation in the ternary complex can be determined experimentally either by NMR spectroscopy or X-ray crystallography. On the basis of this structural information, a linked compound is synthesized in which the ligand for the first site and the ligand for the
- 5 second site are linked. In a preferred embodiment of this type the two ligands are covalently linked. This linked compound is tested to determine if it has a higher binding affinity for the bromodomain than either of the two individual ligands. A linked compound is selected as a ligand when it has a higher binding affinity for the bromodomain than either of the two ligands. In a preferred embodiment the affinity of
- 10 the linked compound with the bromodomain is determined monitoring the ^{15}N - or ^1H -amide chemical shift changes in two dimensional ^{15}N -heteronuclear single-quantum correlation (^{15}N -HSQC) spectra upon the addition of the linked compound to the ^{15}N -labeled bromodomain as described above.
- 15 A larger linked compound can be constructed in an analogous manner, *e.g.*, linking three ligands which bind to three nearby sites on the bromodomain to form a multilinked compound that has an even higher affinity for the bromodomain than the linked compound.

20 Identification of New Bromodomains

- By disclosing that protein bound acetyl-lysine is a binding partner for bromodomains, the present invention provides a method of identifying novel proteins that contain bromodomains. In short, a protein fragment or analog thereof comprising an acetyl-
- 25 lysine can be used as bait to identify a binding partner that comprises a bromodomain. Any one of a number of procedures can be carried out to identify such a binding partner. One such assay comprises passing a cell extract over the bait peptide which is attached to a solid support. After washing the solid support to remove any non-specific binders, the bromodomain containing protein can be eluted from the solid
- 30 support with an appropriate eluant. In a particular embodiment, the free bait peptide can be used in the elution. Other methodology includes the use of a yeast two-hybrid system, a GST pull down assay, ELISA, immunometric assays, and a modification of the CORT procedure of Schlessinger *et al.*, (US Patent No. 5,858,686, Issued on

January 12, 1999 which is hereby incorporated by reference in its entirety) for use with the bromodomain-acetyl-lysine binding complex.

Labels:

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Suitable labels include enzymes, fluorophores (*e.g.*, fluorescein isothiocyanate (FITC), phycoerythrin (PE), Texas red (TR), rhodamine, free or chelated lanthanide series salts, especially Eu^{3+} , to name a few fluorophores), chromophores, radioisotopes, chelating agents, dyes, colloidal gold, latex particles, ligands (*e.g.*, biotin), and

10 chemiluminescent agents. When a control marker is employed, the same or different labels may be used for the test and control marker gene.

In the instance where a radioactive label, such as the isotopes ^3H , ^{14}C , ^{32}P , ^{35}S , ^{36}Cl , ^{51}Cr , ^{57}Co , ^{58}Co , ^{59}Fe , ^{90}Y , ^{125}I , ^{131}I , and ^{186}Re are used, known currently available

15 counting procedures may be utilized. In the instance where the label is an enzyme, detection may be accomplished by any of the presently utilized colorimetric, spectrophotometric, fluorospectrophotometric, amperometric or gasometric techniques known in the art.

20 Direct labels are one example of labels which can be used according to the present invention. A direct label has been defined as an entity, which in its natural state, is readily visible, either to the naked eye, or with the aid of an optical filter and/or applied stimulation, *e.g.* U.V. light to promote fluorescence. Among examples of colored labels, which can be used according to the present invention, include metallic sol

25 particles, for example, gold sol particles such as those described by Leuving (U.S. Patent 4,313,734); dye sol particles such as described by Gribnau *et al.* (U.S. Patent 4,373,932 and May *et al.* (WO 88/08534); dyed latex such as described by May, *supra*, Snyder (EP-A 0 280 559 and 0 281 327); or dyes encapsulated in liposomes as described by Campbell *et al.* (U.S. Patent 4,703,017). Other direct labels include a

30 radionucleotide, a fluorescent moiety or a luminescent moiety. In addition to these direct labeling devices, indirect labels comprising enzymes can also be used according to the present invention. Various types of enzyme linked immunoassays are well known in the art, for example, alkaline phosphatase and horseradish peroxidase,

lysozyme, glucose-6-phosphate dehydrogenase, lactate dehydrogenase, urease, these and others have been discussed in detail by Eva Engvall in Enzyme Immunoassay ELISA and EMIT in *Methods in Enzymology*, **70**:419-439 (1980) and in U.S. Patent 4,857,453.

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Suitable enzymes include, but are not limited to, alkaline phosphatase, β -galactosidase, green fluorescent protein and its derivatives, luciferase, and horseradish peroxidase.

Other labels for use in the invention include magnetic beads or magnetic resonance
10 imaging labels.

Antibodies to Portions of the Bromodomain that Interact with Acetyl-Lysine

According to the present invention, the bromodomains, and more particularly the ZA
15 loops of the bromodomains and fragments thereof can be produced by a recombinant source, or through chemical synthesis, or through the modification of these peptides and fragments; and derivatives or analogs thereof, including fusion proteins, may be used as an immunogen to generate antibodies that specifically interfere with the formation of the bromodomain-acetyl-lysine binding complex. Similarly, antibodies
20 can be raised against peptides that comprise one or more acetyl-lysine residues which also interfere with the formation of the bromodomain-acetyl-lysine binding complex. Such antibodies include but are not limited to polyclonal, monoclonal, chimeric, single chain, Fab fragments, and a Fab expression library.

25 Various procedures known in the art may be used for the production of the polyclonal antibodies. For the production of antibody, various host animals can be immunized by injection with the peptide having the amino acid sequence of SEQ ID NO:3, for example, or a derivative (*e.g.*, or fusion protein) thereof, including but not limited to rabbits, mice, rats, sheep, goats, etc. In one embodiment, the peptide can be
30 conjugated to an immunogenic carrier, *e.g.*, bovine serum albumin (BSA) or keyhole limpet hemocyanin (KLH). Various adjuvants may be used to increase the immunological response, depending on the host species, including but not limited to Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface

active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (*bacille Calmette-Guerin*) and *Corynebacterium parvum*.

- 5 For preparation of monoclonal antibodies directed toward the peptides or protein fragments of the present invention, or analog, or derivative thereof, any technique that provides for the production of antibody molecules by continuous cell lines in culture may be used. These include but are not limited to the hybridoma technique originally developed by Kohler and Milstein [*Nature*, **256**:495-497 (1975)], as well as the trioma
- 10 technique, the human B-cell hybridoma technique [Kozbor *et al.*, *Immunology Today*, **4**:72 (1983); Cote *et al.*, *Proc. Natl. Acad. Sci. U.S.A.*, **80**:2026-2030 (1983)], and the EBV-hybridoma technique to produce human monoclonal antibodies [Cole *et al.*, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96 (1985)]. In an additional embodiment of the invention, monoclonal antibodies can be produced in
- 15 germ-free animals utilizing technology described in PCT/US90/02545. In fact, according to the invention, techniques developed for the production of "chimeric antibodies" [Morrison *et al.*, *J. Bacteriol.*, **159**:870 (1984); Neuberger *et al.*, *Nature*, **312**:604-608 (1984); Takeda *et al.*, *Nature*, **314**:452-454 (1985)] by splicing the genes from a mouse antibody molecule specific for the peptide having the amino acid
- 20 sequence of SEQ ID NO:3, for example, together with genes from a human antibody molecule of appropriate biological activity can be used; such antibodies are within the scope of this invention. Such human or humanized chimeric antibodies are preferred for use in therapy of human diseases or disorders (described *infra*), since the human or humanized antibodies are much less likely than xenogenic antibodies to induce an
- 25 immune response, in particular an allergic response, themselves.

According to the invention, techniques described for the production of single chain antibodies [U.S. Patent Nos. 5,476,786 and 5,132,405 to Huston; U.S. Patent 4,946,778] can be adapted to produce specific single chain antibodies. An additional

- 30 embodiment of the invention utilizes the techniques described for the construction of Fab expression libraries [Huse *et al.*, *Science*, **246**:1275-1281 (1989)] to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity.

Antibody fragments which contain the idiotype of the antibody molecule can be generated by known techniques. For example, such fragments include but are not limited to: the $F(ab')_2$ fragment which can be produced by pepsin digestion of the antibody molecule; the Fab' fragments which can be generated by reducing the disulfide bridges of the $F(ab')_2$ fragment, and the Fab fragments which can be generated by treating the antibody molecule with papain and a reducing agent.

In the production of antibodies, screening for the desired antibody can be accomplished by techniques known in the art, *e.g.*, radioimmunoassay, ELISA (enzyme-linked immunosorbant assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitin reactions, immunodiffusion assays, *in situ* immunoassays (using colloidal gold, enzyme or radioisotope labels, for example), western blots, precipitation reactions, agglutination assays (*e.g.*, gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc. In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labeled. Many means are known in the art for detecting binding in an immunoassay and are within the scope of the present invention. For example, to select antibodies which recognize a specific epitope of a ZA loop of a bromodomain, for example, one may assay generated hybridomas for a product which binds to a bromodomain fragment containing such an epitope and choose those which do not cross-react with bromodomain fragments that do not include that epitope.

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In a specific embodiment, antibodies that interfere with the formation of the bromodomain-acetyl-lysine complex can be generated. Such antibodies can be tested using the assays described and could potentially be used in anti-cancer therapies.

30

Administration

According to the invention, the component or components of a therapeutic composition, *e.g.*, an agent of the invention that interferes with the bromodomain-

acetyl-lysine binding complex such as the peptide having the amino acid sequence of SEQ ID NOs:4, 5, or 6 and a pharmaceutically acceptable carrier, may be introduced parenterally, transmucosally, *e.g.*, orally, nasally, or rectally, or transdermally.

Preferably, administration is parenteral, *e.g.*, via intravenous injection, and also including, but is not limited to, intra-arteriole, intramuscular, intradermal, subcutaneous, intraperitoneal, intraventricular, and intracranial administration.

In a preferred aspect, the agent of the present invention can cross cellular and nuclear membranes, which would allow for intravenous or oral administration. Strategies are available for such crossing, including but not limited to, increasing the hydrophobic nature of a molecule; introducing the molecule as a conjugate to a carrier, such as a ligand to a specific receptor, targeted to a receptor; and the like.

The present invention also provides for conjugating targeting molecules to such an agent. "Targeting molecule" as used herein shall mean a molecule which, when administered *in vivo*, localizes to desired location(s). In various embodiments, the targeting molecule can be a peptide or protein, antibody, lectin, carbohydrate, or steroid. In one embodiment, the targeting molecule is a peptide ligand of a receptor on the target cell. In a specific embodiment, the targeting molecule is an antibody. Preferably, the targeting molecule is a monoclonal antibody. In one embodiment, to facilitate crosslinking the antibody can be reduced to two heavy and light chain heterodimers, or the F(ab')₂ fragment can be reduced, and crosslinked to the agent via the reduced sulfhydryl. Antibodies for use as targeting molecule are specific for a cell surface antigen.

In another embodiment, the therapeutic compound can be delivered in a vesicle, in particular a liposome [*see* Langer, *Science*, **249**:1527-1533 (1990); Treat *et al.*, in *Liposomes in the Therapy of Infectious Disease and Cancer*, Lopez-Berestein and Fidler (eds.), Liss: New York, pp. 353-365 (1989); Lopez-Berestein, *ibid.*, pp. 317-327; see generally *ibid.*].

In yet another embodiment, the therapeutic compound can be delivered in a controlled release system. For example, the agent may be administered using intravenous

infusion, an implantable osmotic pump, a transdermal patch, liposomes, or other modes of administration. In one embodiment, a pump may be used [see Langer, *supra*; Sefton, *CRC Crit. Ref. Biomed. Eng.*, **14**:201 (1987); Buchwald *et al.*, *Surgery*, **88**:507 (1980); Saudek *et al.*, *N. Engl. J. Med.*, **321**:574 (1989)]. In another embodiment,

5 polymeric materials can be used [see *Medical Applications of Controlled Release*, Langer and Wise (eds.), CRC Press: Boca Raton, Florida (1974); *Controlled Drug Bioavailability, Drug Product Design and Performance*, Smolen and Ball (eds.), Wiley: New York (1984); Ranger and Peppas, *J. Macromol. Sci. Rev. Macromol. Chem.*, **23**:61 (1983); see also Levy *et al.*, *Science*, **228**:190 (1985); During *et al.*, *Ann.*

10 *Neurol.*, **25**:351 (1989); Howard *et al.*, *J. Neurosurg.*, **71**:105 (1989)]. In yet another embodiment, a controlled release system can be placed in proximity of the therapeutic target, *i.e.*, the bone marrow, thus requiring only a fraction of the systemic dose [see, *e.g.*, Goodson, in *Medical Applications of Controlled Release, supra*, vol. 2, pp. 115-138 (1984)]. Other controlled release systems are discussed in the review by Langer

15 [*Science*, **249**:1527-1533 (1990)].

Pharmaceutical Compositions. In yet another aspect of the present invention, provided are pharmaceutical compositions of the above. Such pharmaceutical compositions may be for administration for injection, or for oral, pulmonary, nasal or other forms of

20 administration. In general, comprehended by the invention are pharmaceutical compositions comprising effective amounts of a low molecular weight component or components, or derivative products, of the invention together with pharmaceutically acceptable diluents, preservatives, solubilizers, emulsifiers, adjuvants and/or carriers. Such compositions include diluents of various buffer content (*e.g.*, Tris-HCl, acetate,

25 phosphate), pH and ionic strength; additives such as detergents and solubilizing agents (*e.g.*, Tween 80, Polysorbate 80), anti-oxidants (*e.g.*, ascorbic acid, sodium metabisulfite), preservatives (*e.g.*, Thimersol, benzyl alcohol) and bulking substances (*e.g.*, lactose, mannitol); incorporation of the material into particulate preparations of polymeric compounds such as polylactic acid, polyglycolic acid, etc. or into liposomes.

30 Hylauronic acid may also be used. Such compositions may influence the physical state, stability, rate of *in vivo* release, and rate of *in vivo* clearance of the present proteins and derivatives. See, *e.g.*, Remington's Pharmaceutical Sciences, 18th Ed. [1990, Mack Publishing Co., Easton, PA 18042] pages 1435-1712 which are herein

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incorporated by reference. The compositions may be prepared in liquid form, or may be in dried powder, such as lyophilized form.

Oral Delivery. Contemplated for use herein are oral solid dosage forms, which are described generally in Remington's Pharmaceutical Sciences, 18th Ed. 1990 (Mack Publishing Co. Easton PA 18042) at Chapter 89, which is herein incorporated by reference. Solid dosage forms include tablets, capsules, pills, troches or lozenges, cachets or pellets. Also, liposomal or proteinoid encapsulation may be used to formulate the present compositions (as, for example, proteinoid microspheres reported in U.S. Patent No. 4,925,673). Liposomal encapsulation may be used and the liposomes may be derivatized with various polymers (e.g., U.S. Patent No. 5,013,556). A description of possible solid dosage forms for the therapeutic is given by Marshall, K. In: *Modern Pharmaceutics* Edited by G.S. Banker and C.T. Rhodes Chapter 10, 1979, herein incorporated by reference. In general, the formulation will include an agent of the present invention (or chemically modified forms thereof) and inert ingredients which allow for protection against the stomach environment, and release of the biologically active material in the intestine.

Also specifically contemplated are oral dosage forms of the above derivatized component or components. The component or components may be chemically modified so that oral delivery of the derivative is efficacious. Generally, the chemical modification contemplated is the attachment of at least one moiety to the component molecule itself, where said moiety permits (a) inhibition of proteolysis; and (b) uptake into the blood stream from the stomach or intestine. Also desired is the increase in overall stability of the component or components and increase in circulation time in the body. An example of such a moiety is polyethylene glycol.

For the component (or derivative) the location of release may be the stomach, the small intestine (the duodenum, the jejunum, or the ileum), or the large intestine. One skilled in the art has available formulations which will not dissolve in the stomach, yet will release the material in the duodenum or elsewhere in the intestine. Preferably, the release will avoid the deleterious effects of the stomach environment, either by

protection of the protein (or derivative) or by release of the biologically active material beyond the stomach environment, such as in the intestine.

The therapeutic can be included in the formulation as fine multi-particulates in the form of granules or pellets of particle size about 1 mm. The formulation of the material for capsule administration could also be as a powder, lightly compressed plugs or even as tablets. The therapeutic could be prepared by compression.

One may dilute or increase the volume of the therapeutic with an inert material. These diluents could include carbohydrates, especially mannitol, α -lactose, anhydrous lactose, cellulose, sucrose, modified dextrans and starch. Certain inorganic salts may be also be used as fillers including calcium triphosphate, magnesium carbonate and sodium chloride. Some commercially available diluents are Fast-Flo, Emdex, STA-Rx 1500, Emcompress and Avicell.

Disintegrants may be included in the formulation of the therapeutic into a solid dosage form. Materials used as disintegrates include but are not limited to starch, including the commercial disintegrant based on starch, Explotab. Binders also may be used to hold the therapeutic agent together to form a hard tablet and include materials from natural products such as acacia, tragacanth, starch and gelatin.

An anti-frictional agent may be included in the formulation of the therapeutic to prevent sticking during the formulation process. Lubricants may be used as a layer between the therapeutic and the die wall. Glidants that might improve the flow properties of the drug during formulation and to aid rearrangement during compression also might be added. The glidants may include starch, talc, pyrogenic silica and hydrated silicoaluminate.

In addition, to aid dissolution of the therapeutic into the aqueous environment a surfactant might be added as a wetting agent. Additives which potentially enhance uptake of the protein (or derivative) are for instance the fatty acids oleic acid, linoleic acid and linolenic acid.

Nasal Delivery. Nasal delivery of an agent of the present invention (or derivative) is also contemplated. Nasal delivery allows the passage of a peptide, for example, to the blood stream directly after administering the therapeutic product to the nose, without the necessity for deposition of the product in the lung. Formulations for nasal delivery
5 include those with dextran or cyclodextran.

Transdermal administration. Various and numerous methods are known in the art for transdermal administration of a drug, *e.g.*, via a transdermal patch. Transdermal patches are described in for example, U.S. Patent No. 5,407,713, issued April 18, 1995
10 to Rolando *et al.*; U.S. Patent No. 5,352,456, issued October 4, 1994 to Fallon *et al.*; U.S. Patent No. 5,332,213 issued August 9, 1994 to D'Angelo *et al.*; U.S. Patent No. 5,336,168, issued August 9, 1994 to Sibalis; U.S. Patent No. 5,290,561, issued March 1, 1994 to Farhadieh *et al.*; U.S. Patent No. 5,254,346, issued October 19, 1993 to Tucker *et al.*; U.S. Patent No. 5,164,189, issued November 17, 1992 to Berger *et al.*;
15 U.S. Patent No. 5,163,899, issued November 17, 1992 to Sibalis; U.S. Patent Nos. 5,088,977 and 5,087,240, both issued February 18, 1992 to Sibalis; U.S. Patent No. 5,008,110, issued April 16, 1991 to Benecke *et al.*; and U.S. Patent No. 4,921,475, issued May 1, 1990 to Sibalis, the disclosure of each of which is incorporated herein by reference in its entirety.

20 It can be readily appreciated that a transdermal route of administration may be enhanced by use of a dermal penetration enhancer, *e.g.*, such as enhancers described in U.S. Patent No. 5,164,189 (*supra*), U.S. Patent No. 5,008,110 (*supra*), and U.S. Patent No. 4,879,119, issued November 7, 1989 to Aruga *et al.*, the disclosure of each of
25 which is incorporated herein by reference in its entirety.

Pulmonary Delivery. Also contemplated herein is pulmonary delivery of the pharmaceutical compositions of the present invention. A pharmaceutical composition of the present invention is delivered to the lungs of a mammal while inhaling and
30 traverses across the lung epithelial lining to the blood stream. Other reports of this include Adjei *et al.* [*Pharmaceutical Research*, 7:565-569 (1990); Adjei *et al.*, *International Journal of Pharmaceutics*, 63:135-144 (1990) (leuprolide acetate); Braquet *et al.*, *Journal of Cardiovascular Pharmacology*, 13(suppl. 5):143-146 (1989)

(endothelin-1); Hubbard *et al.*, *Annals of Internal Medicine*, **Vol. III**, pp. 206-212 (1989) (α 1-antitrypsin); Smith *et al.*, *J. Clin. Invest.*, **84**:1145-1146 (1989) (α -1-proteinase); Oswein *et al.*, "Aerosolization of Proteins", *Proceedings of Symposium on Respiratory Drug Delivery II*, Keystone, Colorado, March, (1990) (recombinant human growth hormone); Debs *et al.*, *J. Immunol.*, **140**:3482-3488 (1988) (interferon- γ and tumor necrosis factor alpha); Platz *et al.*, U.S. Patent No. 5,284,656 (granulocyte colony stimulating factor)]. A method and composition for pulmonary delivery of drugs for systemic effect is described in U.S. Patent No. 5,451,569, issued September 19, 1995 to Wong *et al.*

10

A subject in whom administration of an agent of the present invention is an effective therapeutic regiment for cancer, for example, is preferably a human, but can be any animal. Thus, as can be readily appreciated by one of ordinary skill in the art, the methods and pharmaceutical compositions of the present invention are particularly suited to administration to any animal, *e.g.*, for veterinary medical use, particularly for a mammal, and including, but by no means limited to, domestic animals, such as feline or canine subjects, farm animals, including bovine, equine, caprine, ovine, and porcine subjects, wild animals (whether in the wild or in a zoological garden), research animals, such as mice, rats, rabbits, goats, sheep, pigs, dogs, cats, avian species, such as chickens, turkeys, and songbirds.

20

The present invention may be better understood by reference to the following non-limiting Example, which is provided as exemplary of the invention. The following example is presented in order to more fully illustrate the preferred embodiments of the invention. It should in no way be construed, however, as limiting the broad scope of the invention.

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EXAMPLE
STRUCTURE AND LIGAND OF A HISTONE
ACETYLTRANSFERASE BROMODOMAIN

5 Introduction

The bromodomain is a protein motif comprising approximately 110 amino acids that is found in practically all nuclear histone acetyltransferases (HATs) [Jeanmougin *et al.*, Trends in Biochemical Sciences, **22**:151-153 (1997)]. However, despite the seemingly requisite occurrence of this motif in HATs, their role in these enzymes is unknown.

10 Indeed, although this motif has also been identified in other chromatin proteins, heretofore not even one binding partner for a bromodomain had been identified.

Materials and Methods

Sample preparation: The bromodomain of P/CAF (residues 719-832 of SEQ ID NO:2) was subcloned into the pET14b expression vector (Novagen) and expressed in *Escherichia coli* BL21(DE3) cells. Uniformly ^{15}N - and $^{15}\text{N}/^{13}\text{C}$ -labelled proteins were prepared by growing bacteria in a minimal medium containing $^{15}\text{NH}_4\text{Cl}$ with or without $^{13}\text{C}_6$ -glucose. A uniformly $^{15}\text{N}/^{13}\text{C}$ -labelled and fractionally deuterated protein sample was prepared by growing the cells in 75% $^2\text{H}_2\text{O}$. The bromodomain was purified by affinity chromatography on a nickel-IDA column (Invitrogen) followed by the removal of poly-His tag by thrombin cleavage. The final purification of the protein was achieved by size-exclusion chromatography. The acetyl-lysine-containing peptides were prepared on a MilliGen 9050 peptide synthesizer (Perkin Elmer) using Fmoc/HBTU chemistry. Acetyl-lysine was incorporated using the reagent Fmoc-Ac-Lys with HBTU/DIPEA activation. NMR samples contained approximately 1 mM protein in 100mM phosphate buffer of pH 6.5 and 5mM perdeuterated DTT and 0.5mM EDTA in $\text{H}_2\text{O}/^2\text{H}_2\text{O}$ (9/1) or $^2\text{H}_2\text{O}$.

NMR spectroscopy: All NMR spectra were acquired at 30°C on a Bruker DRX600 or DRX500 spectrometer. The backbone assignments of the ^1H , ^{13}C , and ^{15}N resonances were achieved using deuterium-decoupled triple-resonance experiments of HNCACB and HN(CO)CACB [Yamazaki *et al.*, *J. Am. Chem. Soc.* **116**:11655-11666 (1994)] recorded using the uniformly $^{15}\text{N}/^{13}\text{C}$ -labeled and fractionally deuterated protein. The

side-chain atoms were assigned from 3D HCCH-TOCSY [Clore and Gronenborn, *Meth. Enzymol.* **239**:249-363 (1994)] and (H)C(CO)NH-TOCSY [Logan *et al.*, *J. Biomol. NMR* **3**:225-231 (1993)] data collected on the uniformly $^{15}\text{N}/^{13}\text{C}$ -labeled protein. Stereospecific assignments of methyl groups of the Val and Leu residues were
5 obtained using a fractionally ^{13}C -labeled sample [Neri *et al.*, *Biochemistry* **28**:7510-7516 (1989)]. The NOE-derived distance restraints were obtained from ^{15}N - or ^{13}C -edited 3D NOESY spectra. ϕ -angle restraints were determined based on the $^3J_{\text{HN,H}\alpha}$ coupling constants measured in a 3D HNHA spectrum [Clore and Gronenborn, *Meth. Enzymol.* **239**:249-363 (1994)]. Slowly exchanging amide protons were
10 identified from a series of 2D ^{15}N -HSQC spectra recorded after the H_2O buffer was changed to a $^2\text{H}_2\text{O}$ buffer. The intermolecular NOEs used in defining the structure of the bromodomain/Ac-histamine complex were detected in ^{13}C -edited (F_1), $^{13}\text{C}/^{15}\text{N}$ -filtered (F_3) 3D NOESY spectrum [Clore and Gronenborn, *Meth. Enzymol.* **239**:249-363 (1994)]. All NMR spectra were processed with the NMRPipe/NMRDraw
15 programs and analyzed using NMRView [Johnson and Blevins, *J. Biomol., NMR* **4**:603-614 (1994)].

Structure calculations: Structures of the bromodomain were calculated with a distance geometry/simulated annealing protocol using the X-PLOR program [Brunger, A. *X-PLOR Version 3.1: A system for X-Ray crystallography and NMR*, Yale University Press, New Haven, CT, (1993)]. A total of 1324 manually assigned NOE-derived
20 distance restraints were obtained from the ^{15}N - and ^{13}C -edited NOE spectra. Further analysis of the NOE spectra was carried out by the iterative automated assignment procedure using ARIA [Nilges and O'Donoghue, *Prog. NMR Spectroscopy* **32**:107-139
25 (1998)], which integrates with X-PLOR for structure calculations. A total of 1519 unambiguous and 590 ambiguous distance restraints were identified from the NOE data by ARIA, many of which were checked and confirmed manually. The ARIA-assigned distance restraints were in agreement with the structures calculated using only the manually assigned NOE distance restraints, 28 hydrogen-bond distance
30 restraints for 14 hydrogen bonds, and 54 ϕ -angle restraints. The final structure calculations employed a total of 3515 NMR experimental restraints obtained from the manual and the ARIA-assisted assignments, 2843 of which were unambiguously assigned NOE-derived distance restraints that comprise of 1077 intra-residue, 621

sequential, 550 medium-range, and 595 long-range NOEs. For the ensemble of the final 30 structures, no distance and torsional angle restraints were violated by more than 0.3 Å and 5°, respectively. The total, distance violation, and dihedral violation energies were 178.7 ± 2.4 kcal mol⁻¹, 41.6 ± 0.9 kcal mol⁻¹, and 0.50 ± 0.06 kcal mol⁻¹, respectively. The Lennard-Jones potential which was not used during any refinement stage, was -526.2 ± 16.8 kcal mol⁻¹ for the final structures. Ramachandran plot analysis of the final structures (residues 727-828) with Procheck-NMR [Laskowski *et al.*, *J. Biomol. NMR* **8**:477-486 (1996)] showed that $71.0 \pm 0.6\%$, $23.8 \pm 0.6\%$, $3.5 \pm 0.2\%$, and $1.7 \pm 0.2\%$ of the non-Gly and non-Pro residues were in the most favorable, additionally allowed, generously allowed, and disallowed regions, respectively. The corresponding values for the residues in the four α -helices (residues 727-743, 770-776, 785-802, and 807-827) were $88.9 \pm 0.4\%$, $11.0 \pm 0.4\%$, $0.1 \pm 0.1\%$, and $0.0 \pm 0.0\%$, respectively. The structure of the bromodomain/acetyl-histamine complex was determined using the free form structure and additional 25 intermolecular and 5 intra-ligand NOE-derived distance restraints.

Site-directed mutagenesis: Mutant proteins were prepared using the QuickChange site-directed mutagenesis kit (Stratagene). The presence of appropriate mutations was confirmed by DNA sequencing.

Ligand titration: Ligand titration experiments were performed by recording a series of 2D ¹⁵N- and ¹³C-HSQC spectra on the uniformly ¹⁵N-, and ¹⁵N/¹³C-labelled bromodomain (~0.3mM), respectively, in the presence of different amounts of ligand concentration ranging from 0 to approximately 2.0 mM. The protein sample and the stock solutions of the ligands were all prepared in the same aqueous buffer containing 100mM phosphate and 5mM perdeuterated DTT at pH 6.5.

The full length nucleic acid sequence of the human p300/CBP-associated factor (P/CAF) was obtained from GenBank. Accession No: U57317.2 (SEQ ID NO:1) :

```

1  gggggcgcgt  cgacgcggaa aagaggccgt ggggggcctc ccagcgctgg cagacaccgt
61  gaggctggca gccgccggca cgcacacctg gtccgcagtc ccgaggaaca tgtccgcagc
121  cagggcgcg  agcagagtcc cgggcaggag aaccaaggga gggcgtgtgc tgtggcggcg
181  gcggcagcgg cagcggagcc gctagtcccc tccctcctgg gggagcagct gccgccgctg
241  ccgccgcgcg caccaccatc agcgcgcggg gcccggccag agcgagccgg gcgagcggcg

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40

2941 gattaattga caagtgattt tttttccccc tctgcttctt agaaactcac caagcagtgt
3001 gcctaaagca aggt

The full length protein sequence of the human p300/CBP-associated factor (P/CAF)

5 was obtained from GenBank. Accession No: U57317.2, (SEQ ID NO:2):

1 MSEAGGAGPG GCGAGAGAGA GPGALPPQPA ALPPAPPQGS PCAAAGGSG ACGPATAVAA
61 AGTAEGPGGG GSARIAVKA QLRAPRAKK LEKLGVSAC KAEESCKNG WKNPNPSPTP
121 PRADLQQIIV SLTESCRSCS HALAAHVSHL ENVSEEMNR LLGIVLDVEY LFTCVHKEED
181 ADTKQVYFYL FKLLRKSILQ RGKPVVEGSL EKKPPFEKPS IEQGVNNFVQ YKFSHLPAGE
10 241 RQTIVELAKM FLNRINYWHL EAPSQRRLRS PNDDISGYKE NYTRWLCYCN VPQFCDLPR
301 YETTQVFGRT LLRSVFTVMR RQLLEQARQE KDKLPLEKRT LILTHFPKFL SMLEEEVYSQ
361 NSPIWDQDFL SASSRTSQLG IQTVINPPPV AGTISYNSTS SSLEQPNAGS SSPACKASSG
421 LEANPGEKRR MTDSHVLEE KPRVMGDIP MELINEVMST ITDPAAMLGP ETNFLSAHSA
481 RDEAARLEER RGVIEFHVVG NSLNQKPNKK ILMWLVLQON VFSHQLPRMP KEYITRLVFD
15 541 PKHKTALIK DGRVIGGICF RMFPSQGFTE IVFCAVTSNE QVKGYGTHLM NHLKEYHIKH
601 DILNFLTLYAD EYAIGYFKKQ GFSKEIKIPK TKYVGVIKDY EGATLMGCEL NPRIPYTEFS
661 VIIKKQKEII KKLIERKQAG IRKVYPGLSC FKDGVRQIPI ESIPGIRETG WKPSGKEKSK
721 EPRDPDQLYS TLKSILQQVK SHQSAWPFME PVKRTEAPGY YEVIKFPMDL KTMSEKLNK
781 YYVSKKLFMA DLQRVFTNCK EYNAAESEYY KANILEKFF FSKIKEAGLI DK
20

Results

The P/CAF bromodomain represents an extensive family of bromodomains (Figure 1). A large number of long-range nuclear Overhauser enhancement (NOE)-derived
25 distance restraints were identified in the NMR data of the P/CAF bromodomain, yielding a well-defined three-dimensional structure (Figures 2A -2D). Table 1 shows the NMR chemical shift assignment of the P/CAF bromodomain. Table 2 shows the Unambiguous NOE-derived distance restraints. Table 3 shows the Ambiguous NOE-derived distance restraints. Table 4 shows the Hydrogen bond restraints. The NMR
30 structure coordinates of the P/CAF bromodomain in the free and complexed to acetyl-histamine are shown in Tables 5 and 6, respectively.

The structure consists of a four-helix bundle (helices α_Z , α_A , α_B , and α_C) with a left-handed twist, and a long intervening loop between helices α_Z and α_A (termed the
35 ZA loop, Figure 2E). The four amphipathic α -helices are packed tightly against one another in an antiparallel manner, with crossing angles for adjacent helices of ~ 16 - 20° . The up-and-down four-helix bundle can adapt two topological folds with opposite

handedness (Figures 2F-2G). The right-handed four-helix bundle fold occurs more commonly and is seen in proteins such as hemerythrin and cytochrome b_{562} . The left-handed fold of the bromodomain structure is less common, but also observed in proteins such as cytochrome b_5 and T4 lysozyme [Richardson, J., *Adv. Protein Chem.*, **34**:167-339 (1989); Presnell and Cohen, *Proc. Natl. Acad. Sci. USA* **86**:6592-6596 (1989)]. This topological difference arises from the orientation of the loop between the first two helices (Fig. 2F-2G). The right-handed four-helix bundle proteins have a relatively short hairpin-like connection between the first two helices, which makes the “preferred” turn to the right at the top of the first helix [Richardson, J., *Adv. Protein Chem.*, **34**:167-339 (1989); Presnell and Cohen, *Proc. Natl. Acad. Sci. USA* **86**:6592-6596 (1989); Weber and Salemme, *Nature* **287**:82-84 (1980)]. In contrast, proteins with the left-handed fold usually have a long loop after the first helix and often contain additional secondary structural elements at the base of the helix bundle [Richardson, J., *Adv. Protein Chem.*, **34**:167-339 (1989); Presnell and Cohen, *Proc. Natl. Acad. Sci. USA* **86**:6592-6596 (1989)]. In the bromodomain structure, this long ZA loop has a defined conformation and is packed against the loop between helices α_B and α_C (termed the BC loop) to form a hydrophobic pocket. These tertiary interactions between the two loops appear to favor the left turn of the ZA loop, resulting in the left-handed four-helix bundle fold of the bromodomain. The hydrophobic pocket formed by loops ZA and BC is lined by residues Val752, Ala757, Tyr760, Val763, Tyr802 and Tyr809 (Fig. 2H), and appears to be a site for protein-protein interactions (see below). The pocket is located at one end of the four-helix bundle, opposite to the N- and C-termini of the protein. Interestingly, the ZA loop varies in length amongst different bromodomains, but almost always contains residues corresponding to Phe748, Pro751, Pro758, Tyr760, and Pro767 (Figure 1). The conservation of these residues within the ZA loop as well as residues within the α -helical regions implies a similar left-handed four-helix bundle structure for the large family of bromodomains (Fig. 1).

The modular bromodomain structure supports the idea that bromodomain can act as a functional unit for protein-protein interactions. The observation that bromodomains are found in nearly all known nuclear HATs (A-type) that are known to promote transcription-related acetylation of histones on specific lysine residues, but not present in cytoplasmic HATs (B-type), prompted the determination of whether bromodomains

can interact with acetyl-lysine (AcK). The NMR titration of the P/CAF bromodomain were performed with a peptide (SGRGKGG-AcK-GLGK) derived from histone H4, in which Lys8 is acetylated (Lys8 is the major acetylation site in H4 for GCN5, a yeast homologue of P/CAF). Remarkably, the bromodomain could indeed bind the AcK peptide. Moreover, this interaction appeared to be specific, based on the ^{15}N -HSQC spectra which showed that only a limited number of residues underwent chemical shift changes as a function of peptide concentration (Figure 3A). Conversely, the NMR titration of the bromodomain with a non-acetylated, but otherwise identical H4 peptide, showed no noticeable chemical shift changes, demonstrating that the interaction between the bromodomain and the lysine-acetylated H4 peptide was dependent upon acetylation of lysine. The dissociation constant (K_D) for the AcK peptide was estimated to be $346 \pm 54 \mu\text{M}$. This binding is likely reinforced through additional interactions between bromodomain-containing proteins and target proteins. Notably, many chromatin-associated proteins contain two or multiple bromodomains (Figure 1). Indeed, binding with another lysine-acetylated peptide (RKSTGG-AcK-APRKQ) derived from the major acetylation site on histone H3 (residues 9-20) was also observed. Together, these data demonstrate that the P/CAF bromodomain has the ability to bind AcK peptides in an acetylation dependent manner.

Intriguingly, the bromodomain residues that exhibited the most significant ^1H and ^{15}N chemical shift changes on peptide binding are located near the hydrophobic pocket between the ZA and BC loops (Figure 3B). Because a similar pattern of amide chemical shift changes was observed with the two different AcK-containing peptides, it was surmised that the hydrophobic cavity is the primary binding site for AcK. This hypothesis was further supported by titration with acetyl-histamine, which mimics the chemical structure of the AcK side-chain (Figure 3C). Both ^{15}N - and ^{13}C -HSQC spectra showed that interaction with acetyl-histamine was also acetylation-dependent, involving the same set of residues that showed chemical shift perturbations with similar concentration dependence. It should be noted that the bromodomain did not bind to the amino acids acetyl-lysine or acetyl-histidine alone, possibly due to the presence of the charged amino, carboxyl, or carboxylate group adjacent to the acetyl moiety (Figure 3C). Taken together, these results strongly suggest that the P/CAF

bromodomain can interact with acetyl-lysine-containing proteins in a specific manner, and that this interaction is localized to the bromodomain hydrophobic cavity.

- To identify the key residues involved in bromodomain-AcK recognition, the NMR structure of the P/CAF bromodomain in complex with acetyl-histamine was elucidated. As anticipated, the acetylated moiety binds in the bromodomain hydrophobic pocket (Figure 4). The intermolecular interactions are largely hydrophobic in nature, with the methyl group of acetyl-histamine making extensive contacts with the side-chains of Val752, Ala757, and Tyr760, and the methylene groups of acetyl-histamine displaying specific NOEs to Val752, Ala757, Tyr760, Tyr802, and Tyr809. No intermolecular NOEs were observed for the imidazole ring of acetyl-histamine. From the spectral analysis it is clear that the structure of the bromodomain is very similar in both the free and complex forms.
- It is worth noting that the bromodomain-AcK recognition is reminiscent of the interactions between the histone acetyltransferase Hat1 and acetyl-CoA. Although the binding pockets of these two otherwise structurally unrelated proteins are composed of different secondary structural elements, the nature of acetyl-lysine recognition has striking similarities. In particular, Tyr809, Tyr802, Tyr760, and Val752 in the bromodomain appear to be related to Phe220, Phe261, Val254, and Ile217 of Hat1, respectively, in their interactions with the acetyl moiety. This observation may suggest an evolutionary convergent mechanism of acetyl-lysine recognition between bromodomains and histone acetyltransferases.
- To determine the relative contributions of residues within the hydrophobic cavity in bromodomain-AcK binding, site-directed mutagenesis was used to alter residues Tyr809, Tyr802, Tyr760, and Val752 (Table 7).

Table 7. Structural and Functional Analysis of the P/CAF Bromodomain Mutants

5	Bromodomain Proteins	Structural Integrity ^a	H4 AcK-Peptide Binding K_D (μ M) ^b
	Wild-Type	++++	346 \pm 54
	Tyr809Ala	++++	No Binding ^c
10	Tyr802Ala	+++	> 10,000 ^d
	Tyr760Ala	+++	> 10,000
15	Val752Ala	++	> 10,000

a. The effects of mutations on the structural integrity of the bromodomain were assessed by using the ¹⁵N-HSQC spectra. The amide ¹H/¹⁵N resonances of the mutant proteins were compared to those of the wild-type bromodomain to determine if the particular mutations lead to global or local structure disruption. Severe line-broadening of the amide resonances would indicate protein conformational exchange due to a decrease of structure stability resulting from point mutations. Structural integrity of the mutant proteins is expressed here relative to that of the wild-type, using the signs of “++++” for as stable as the wild-type, “+++” for mildly destabilized, “++” for moderately destabilized, and “-” for completely unfolded.

b. The ligand binding affinity (K_D) of the bromodomain proteins was estimated by following chemical shift changes of amide peaks in the ¹⁵N-HSQC spectra as a function of the ligand concentration.

c. No detectable ligand binding observed in the NMR titration.

d. Ligand binding affinity was significantly reduced and beyond the limit for reliable measurements by NMR titration.

Substitution of Ala for Tyr809 completely abrogated the bromodomain binding to the lysine-acetylated H4 peptide, while the Tyr802Ala, Tyr760Ala, and Val752Ala mutants had significantly reduced ligand binding affinity. To assess whether these mutations disrupted the overall bromodomain fold, the ^{15}N -HSQC spectra of the mutants was compared to that of the wild-type protein. For the Tyr809Ala mutant, the amide chemical shifts were only affected for a few residues near the mutation site. However, mutations of the other residues in the hydrophobic binding pocket perturbed the local protein conformation to greater extents, particularly the ZA loop (Table 7). Thus, the NMR structural analysis and the mutagenesis studies show that Tyr809, which is structurally supported by Trp746 and Asn803 (Figure 4), is essential for the bromodomain interaction with the acetyl group of acetyl-lysine, while residues of Tyr802, Tyr760, and Val752 likely play both structural and functional roles in the recognition. These residues are highly conserved throughout the bromodomain family (Figure 1), suggesting that recognition of acetyl-lysine may be a feature of bromodomains, in general. Therefore, Val752, Ala757, Tyr760, Tyr802, Asn803, and Tyr809 are key amino acid residues for the P/CAF bromodomain binding to acetyl-lysine.

Table 8: Amino Acid Sequences of Bromodomains Identified in Figure 1

PROTEIN BD	SEQ ID NO:	GenBank Acc. No.	PROTEIN BD	SEQ ID NO:	GenBank Acc. No.
hsp/CAF	7	U57317	dmFSH-2	25	
hsGCN5	8	U57136	scBDF1-2	26	
ttP55	9	U47321	hsBR140	27	JC2069
scGCN5	10	Q03330	hsSMAP	28	X87613
hsP300	11	A54277	ggPB1-1	29	X90849
hsCBP	12	S39162	ggPB1-2	30	
mmCBP	13	S39161	ggPB1-3	31	
ceYNI1	14	P34545	ggPB1-4	32	
hsCCG1-1	15	P21675	ggPB1-5	33	
msCCG1-1	16	D26114	spBRO-1	34	S54260
hsCCG1-2	17		spBRO-2	35	
msCCG1-2	18		hsSNF2a	36	S45251
hsRing3-1	19	P25440	hsBRG1	37	S39039
hsORFX-1	20	D26362	ggBRM	38	X91638
dmFSH-1	21	P13709	ggBRG1	39	X91637
scBDF1-1	22	P35817	hsTIF1b	40	X97548
hsRing3-2	23		mmTIF1b	41	X99644
hsORFX-2	24		mmTIF1a	42	S78219

The present invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and the accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

It is further to be understood that all base sizes or amino acid sizes, and all molecular weight or molecular mass values, given for nucleic acids or polypeptides are approximate, and are provided for description.

- 5 Various publications are cited herein, the disclosures of which are hereby incorporated by reference herein in their entireties.

WHAT IS CLAIMED IS:

- 1 1. An isolated nucleic acid encoding a peptide consisting of about 21 to 40
2 amino acids comprising a ZA loop of a bromodomain comprising the amino acid
3 sequence of SEQ ID NO:3.
- 1 2. The isolated nucleic acid of Claim 1 further comprising a heterologous
2 nucleotide sequence.
- 1 3. An isolated nucleic acid encoding a peptide consisting of about 21 to 40
2 amino acids comprising a ZA loop of a bromodomain, wherein the bromodomain has
3 an amino acid sequence selected from the group consisting of SEQ ID NOs. 7, 8, 9,
4 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32,
5 33, 34, 35, 36, 37, 38, 39, 40, 41, and 42.
- 1 4. The isolated nucleic acid of Claim 3 further comprising a heterologous
2 nucleotide sequence.
- 1 5. A peptide consisting of about 21 to 40 amino acids comprising a ZA loop of
2 a bromodomain comprising the amino acid sequence of SEQ ID NO:3.
- 1 6. A fusion protein or peptide comprising the peptide of Claim 5.
- 1 7. A peptide consisting of about 21 to 40 amino acids comprising a ZA loop of
2 a bromodomain, wherein the bromodomain has an amino acid sequence selected from
3 the group consisting of SEQ ID NOs. 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20,
4 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, and
5 42.

1 8. A fusion protein or peptide comprising the peptide of Claim 7.

1 9. An antibody raised against the peptide of Claim 7 or raised against an
2 antigenic fragment thereof.

1 10. An antibody raised against the peptide of Claim 5.

1 11. A method of identifying a compound that modulates the affinity of a
2 bromodomain for a ligand that comprises an acetyl-lysine,
3 said method comprising:

4 (a) contacting the bromodomain and the ligand in the presence of the
5 compound, wherein the bromodomain and the ligand bind in the absence of the
6 compound; and

7 (b) measuring the affinity of the bromodomain for the ligand; wherein
8 a compound is identified as a compound that modulates the affinity of the
9 bromodomain for the ligand when there is a change in the affinity of the
10 bromodomain for the ligand in the presence of the compound.

1 12. The method of Claim 11, wherein the affinity of the bromodomain for the
2 ligand increases in the presence of the compound and wherein the compound is
3 identified as a bromodomain-ligand complex promoting agent.

1 13. The method of Claim 11, wherein the affinity of the bromodomain for the
2 ligand decreases in the presence of the compound and the compound is identified as an
3 inhibitor.

1 14. The method of Claim 11, wherein the compound is selected by performing
2 rational drug design with the set of atomic coordinates obtained from one or more of

3 Tables 1-6, wherein said selecting is performed in conjunction with computer
4 modeling.

1 15. The method of Claim 11, wherein the compound is selected by performing
2 rational drug design with the set of atomic coordinates obtained from a set of atomic
3 coordinates defining the three-dimensional structure of a bromodomain consisting of
4 the amino acid sequence of SEQ ID NO:7, wherein said selecting is performed in
5 conjunction with computer modeling.

1 16. A method of identifying a compound that modulates the stability of a
2 bromodomain-acetyl-lysine binding complex comprising:

3 (a) contacting the bromodomain-acetyl-lysine binding complex in the
4 presence of the compound wherein the bromodomain-acetyl-lysine binding complex
5 forms in the absence of the compound; and

6 (c) measuring the stability of the bromodomain-acetyl-lysine binding
7 complex; wherein a compound is identified as a compound that modulates the stability
8 of the bromodomain-acetyl-lysine binding complex, when there is a change in the
9 stability of the bromodomain-acetyl-lysine binding complex in the presence of the
10 compound.

1 17. The method of Claim 16, wherein the stability of the bromodomain-acetyl-
2 lysine binding complex increases in the presence of the compound and wherein the
3 compound is identified as a stabilizing agent.

1 18. The method of Claim 16, wherein the stability of the bromodomain-acetyl-
2 lysine binding complex decreases in the presence of the compound and the compound
3 is identified as an inhibitor.

1 19. The method of Claim 16, wherein the compound is selected by performing
2 rational drug design with the set of atomic coordinates obtained from one or more of
3 Tables 1-6, wherein said selecting is performed in conjunction with computer
4 modeling.

1 20. The method of Claim 16, wherein the compound is selected by performing
2 rational drug design with the set of atomic coordinates obtained from a set of atomic
3 coordinates defining the three-dimensional structure of a bromodomain consisting of
4 the amino acid sequence of SEQ ID NO:7, wherein said selecting is performed in
5 conjunction with computer modeling.

1 21. A method of identifying a binding partner for a protein that comprises an
2 acetyl-lysine said method comprising:

3 (a) contacting the protein with a polypeptide comprising a
4 bromodomain; and

5 (b) determining whether the polypeptide binds to the protein; wherein
6 a binding partner for a protein is identified when polypeptide binds to the protein.

1 22. The method of Claim 21 wherein the bromodomain has an amino acid
2 sequence from selected from the group consisting of SEQ ID NOs. 7, 8, 9, 10, 11, 12,
3 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35,
4 36, 37, 38, 39, 40, 41 and 42.

1 23. An agent that can inhibit the binding of a bromodomain with a protein
2 comprising an acetyl-lysine selected from the group consisting of : ISYGR-AcK-
3 KRRQRR (SEQ ID NO:4), ARKSTGG-AcK-APRKQL (SEQ ID NO:5) and
4 QSTSRHK-AcK-LMFKTE (SEQ ID NO:6).

002220-4-002220

ABSTRACT OF THE INVENTION

5

Table 1

**NMR Chemical
Shift Assignment
of the P/CAF
Bromodomain**

RES_ID	715	HETEROGENEITY	100	CA	62.320000	CG1	28.733000
RES_TYPE	GLY	N	121.192000	HA	4.038000	HG11	1.748000
SPIN_SYSTEM_ID	1	HN	8.416000	CB	38.640000	HG12	1.052000
HETEROGENEITY	100	CA	63.430000	HB1	3.211000	CG2	17.168000
END_RES_DEF		HA	4.331000	HB2	3.024000	HG2#	1.003000
		CB	30.930000	CD1	134.350000	CD1	13.863000
		HB1	1.815000	HD1	7.053000	HD1#	0.619000
		HB2	1.762000	CE1	119.481000	END_RES_DEF	
		CG	27.630000	HE1	6.882000		
		HG1	1.681000	END_RES_DEF		RES_ID	736
		CD	43.603000			RES_TYPE	LEU
		HD1	3.161000			SPIN_SYSTEM_ID	22
		END_RES_DEF				HETEROGENEITY	100
RES_ID	716	RES_ID	724	RES_ID	730	N	119.880000
RES_TYPE	SER	RES_TYPE	ASP	RES_TYPE	SER	HN	8.841000
SPIN_SYSTEM_ID	2	SPIN_SYSTEM_ID	10	SPIN_SYSTEM_ID	16	CA	58.473000
HETEROGENEITY	100	HETEROGENEITY	100	HETEROGENEITY	100	HA	4.090000
END_RES_DEF		N	122.012000	N	112.173000	CB	41.950000
		HN	8.273000	HN	8.167000	HB1	2.090000
		CA	52.415000	HA	3.920000	HB2	1.703000
		HA	4.874000	HB1	3.995000	CG	27.330000
		CB	41.400000	END_RES_DEF		HG	1.759000
		HB1	2.754000	RES_ID	731	CD1	26.530000
		HB2	2.692000	RES_TYPE	THR	HD1#	1.061000
		END_RES_DEF		SPIN_SYSTEM_ID	17	CD2	23.776000
RES_ID	717	END_RES_DEF		HETEROGENEITY	100	HD2#	0.977000
RES_TYPE	HIS	RES_ID	725	N	120.372000	END_RES_DEF	
SPIN_SYSTEM_ID	3	RES_TYPE	PRO	HN	8.059000		
HETEROGENEITY	100	SPIN_SYSTEM_ID	11	CA	66.730000	RES_ID	737
END_RES_DEF		HETEROGENEITY	100	HA	3.924000	RES_TYPE	GLN
		CA	65.080000	CB	68.930000	SPIN_SYSTEM_ID	23
		HA	4.329000	HB	4.247000	HETEROGENEITY	100
		CB	32.590000	CG2	21.570000	N	117.256000
		HB1	2.326000	HG2#	1.142000	HN	8.505000
		HB2	1.973000	END_RES_DEF		CA	59.020000
		CG	27.632000	RES_ID	732	HA	4.032000
		HG1	2.028000	RES_TYPE	LEU	CB	28.182000
		CD	51.310000	SPIN_SYSTEM_ID	18	HB1	2.327000
		HD1	3.866000	HETEROGENEITY	100	HB2	2.263000
		END_RES_DEF		N	120.536000	CG	34.240000
RES_ID	719	RES_ID	726	HN	8.460000	HG1	2.536000
RES_TYPE	SER	RES_TYPE	ASP	CA	57.920000	HG2	2.461000
SPIN_SYSTEM_ID	5	SPIN_SYSTEM_ID	12	HA	3.289000	END_RES_DEF	
HETEROGENEITY	100	HETEROGENEITY	100	CB	39.750000		
END_RES_DEF		N	119.716000	HB1	1.532000	RES_ID	738
		HN	8.397000	HB2	0.294000	RES_TYPE	GLN
		CA	55.720000	CG	24.880000	SPIN_SYSTEM_ID	24
		HA	4.692000	HG	1.683000	HETEROGENEITY	100
		CB	40.550000	CD1	25.429000	N	118.896000
		HB1	2.792000	HD1#	0.469000	HN	8.033000
		HB2	2.730000	CD2	19.921000	CA	59.574000
		END_RES_DEF		HD2#	-0.193000	HA	4.196000
				END_RES_DEF		CB	29.835000
RES_ID	720	RES_ID	727	RES_ID	733	HB1	2.482000
RES_TYPE	LYS	RES_TYPE	GLN	RES_TYPE	LYS	HB2	2.469000
SPIN_SYSTEM_ID	6	SPIN_SYSTEM_ID	13	SPIN_SYSTEM_ID	19	CG	35.342000
HETEROGENEITY	100	HETEROGENEITY	100	HETEROGENEITY	100	HG1	2.840000
CA	56.296000	N	121.356000	N	118.568000	HG2	2.467000
HA	4.361000	HN	8.196000	HN	8.563000	NE2	110.369000
CB	33.140000	CA	55.920000	CA	60.125000	HE21	7.022000
HB1	1.882000	HA	4.163000	HA	3.679000	HE22	6.916000
HB2	1.684000	CB	28.730000	CB	32.588000	END_RES_DEF	
CG	25.430000	HB1	2.148000	HB1	1.729000		
HG1	1.585000	CG	34.240000	HB2	1.360000	RES_ID	739
HG2	1.433000	HG1	2.524000	CG	24.880000	RES_TYPE	VAL
CD	29.834000	HG2	2.371000	HG1	1.280000	SPIN_SYSTEM_ID	25
HD1	1.703000	END_RES_DEF		CD	29.835000	HETEROGENEITY	100
CE	41.960000	RES_ID	728	HD1	1.585000	N	119.716000
HE1	3.003000	RES_TYPE	LEU	CE	41.960000	HN	8.526000
END_RES_DEF		SPIN_SYSTEM_ID	14	HE1	2.918000	CA	67.830000
		HETEROGENEITY	100	END_RES_DEF		HA	3.844000
RES_ID	721	N	121.356000	RES_ID	734	CB	32.030000
RES_TYPE	GLU	HN	8.196000	RES_TYPE	SER	HB	2.384000
SPIN_SYSTEM_ID	7	CA	55.920000	SPIN_SYSTEM_ID	20	CG1	23.330000
HETEROGENEITY	100	HA	4.163000	HETEROGENEITY	100	HG1#	1.183000
N	122.990000	CB	28.730000	N	113.157000	CG2	22.120000
HN	8.317000	HB1	2.148000	HN	7.540000	HG2#	1.033000
CA	54.620000	HB2	1.555000	CA	61.227000	END_RES_DEF	
HA	4.540000	CG	27.080000	HA	4.281000	RES_ID	740
CB	29.830000	HG	1.480000	CB	63.879000	RES_TYPE	LYS
HB1	2.024000	CD1	25.970000	HB1	4.060000	SPIN_SYSTEM_ID	26
HB2	1.893000	HD1#	0.794000	END_RES_DEF		HETEROGENEITY	100
CG	35.893000	CD2	23.226000	RES_ID	735	N	114.633000
HG1	2.271000	HD2#	0.786000	RES_TYPE	ILE	HN	8.572000
END_RES_DEF		END_RES_DEF		SPIN_SYSTEM_ID	21	CA	59.574000
RES_ID	722	RES_ID	729	HETEROGENEITY	100	HA	3.886000
RES_TYPE	PRO	RES_TYPE	TYR	N	120.700000	CB	32.380000
SPIN_SYSTEM_ID	8	SPIN_SYSTEM_ID	15	HN	7.951000	HB1	1.873000
HETEROGENEITY	100	HETEROGENEITY	100	CA	65.080000	HG1	1.022000
CA	63.430000	N	119.060000	HA	3.786000	HD1	1.520000
HA	4.393000	HN	8.021000	CB	38.095000	END_RES_DEF	
CB	32.030000			HB	1.879000	RES_ID	741
HB1	2.224000					RES_TYPE	SER
HB2	1.880000						
CG	27.630000						
HG1	2.028000						
CD	50.760000						
HD2	3.656000						
HD1	3.800000						
END_RES_DEF							

SPIN_SYSTEM_ID 27
 HETEROGENEITY 100
 N 110.369000
 HN 7.557000
 CA 59.024000
 HA 4.448000
 CB 63.980000
 HB1 4.004000
 END_RES_DEF

RES_ID 742
 RES_TYPE HIS
 SPIN_SYSTEM_ID 28
 HETEROGENEITY 100

N 125.619000
 HN 7.536000
 CA 58.473000
 HA 3.967000
 CB 32.588000
 HB1 2.990000
 HB2 2.799000
 CD2 118.930000
 HD2 4.978000
 CE1 138.755000
 HE1 7.522000
 END_RES_DEF

RES_ID 743
 RES_TYPE GLN
 SPIN_SYSTEM_ID 29
 HETEROGENEITY 100

N 128.571000
 HN 8.543000
 CA 59.125000
 HA 4.209000
 CB 29.834000
 HB1 2.111000
 CG 33.690000
 HG1 2.390000
 NE2 112.173000
 HE21 7.581000
 HE22 6.870000
 END_RES_DEF

RES_ID 744
 RES_TYPE SER
 SPIN_SYSTEM_ID 30
 HETEROGENEITY 100

N 119.060000
 HN 11.668000
 CA 60.125000
 HA 4.838000
 CB 63.980000
 HB1 4.334000
 HB2 3.926000
 END_RES_DEF

RES_ID 745
 RES_TYPE ALA
 SPIN_SYSTEM_ID 31
 HETEROGENEITY 100

N 117.584000
 HN 7.868000
 CA 53.510000
 HA 4.396000
 CB 20.470000
 HB# 1.688000
 END_RES_DEF

RES_ID 746
 RES_TYPE TRP
 SPIN_SYSTEM_ID 32
 HETEROGENEITY 100

N 116.600000
 HN 7.135000
 CA 60.691000
 HA 4.368000
 CB 27.630000
 HB1 3.594000
 HB2 3.351000
 CD1 128.843000
 HD1 7.897000
 NE1 110.861000
 HE1 10.474000
 CE3 122.234000
 HE3 7.336000
 CZ2 116.177000
 HZ2 7.382000
 CZ3 123.336000
 HZ3 7.197000
 CH2 126.089000
 HH2 7.150000
 END_RES_DEF

RES_ID 747

RES_TYPE PRO
 SPIN_SYSTEM_ID 33
 HETEROGENEITY 100

CA 64.531000
 HA 3.756000
 CB 29.835000
 HB1 0.487000
 HB2 -0.783000
 CG 26.530000
 HG1 0.233000
 HG2 -0.931000
 CD 50.212000
 HD2 1.567000
 HD1 2.177000
 END_RES_DEF

RES_ID 748
 RES_TYPE PHE
 SPIN_SYSTEM_ID 34
 HETEROGENEITY 100

N 113.321000
 HN 7.585000
 CA 55.719000
 HA 4.930000
 CB 39.202000
 HB1 3.491000
 HB2 2.532000
 CD1 133.248000
 HD1 7.099000
 HE1 7.174000
 HZ 7.296000
 END_RES_DEF

RES_ID 749
 RES_TYPE MET
 SPIN_SYSTEM_ID 35
 HETEROGENEITY 100

N 117.748000
 HN 7.115000
 CA 56.820000
 HA 4.286000
 CB 32.590000
 HB1 2.233000
 HB2 2.174000
 CG 33.140000
 HG1 2.851000
 CE 17.168000
 HE# 2.175000
 END_RES_DEF

RES_ID 750
 RES_TYPE GLU
 SPIN_SYSTEM_ID 36
 HETEROGENEITY 100

N 113.813000
 HN 7.709000
 CA 53.516000
 HA 4.849000
 CB 31.487000
 HB1 2.091000
 HB2 1.730000
 CG 35.893000
 HG1 2.164000
 END_RES_DEF

RES_ID 751
 RES_TYPE PRO
 SPIN_SYSTEM_ID 37
 HETEROGENEITY 100

CA 62.879000
 HA 4.242000
 CB 32.040000
 HB1 2.328000
 HB2 1.683000
 CG 27.080000
 HG1 2.126000
 HG2 1.978000
 CD 50.763000
 HD1 3.670000
 END_RES_DEF

RES_ID 752
 RES_TYPE VAL
 SPIN_SYSTEM_ID 38
 HETEROGENEITY 100

N 124.450000
 HN 8.124000
 CA 63.430000
 HA 3.553000
 CB 32.580000
 HB 1.145000
 CG1 21.573000
 HG1# 0.464000
 CG2 21.573000
 HG2# 0.169000

END_RES_DEF

RES_ID 753
 RES_TYPE LYS
 SPIN_SYSTEM_ID 39
 HETEROGENEITY 100

N 129.883000
 HN 9.045000
 CA 56.310000
 HA 4.370000
 CB 32.880000
 HB1 1.873000
 HG1 1.435000
 HD1 1.673000
 HE1 2.985000
 END_RES_DEF

RES_ID 754
 RES_TYPE ARG
 SPIN_SYSTEM_ID 40
 HETEROGENEITY 100

N 120.208000
 HN 8.054000
 END_RES_DEF

RES_ID 755
 RES_TYPE THR
 SPIN_SYSTEM_ID 41
 HETEROGENEITY 100

CA 63.430000
 HA 4.038000
 CB 68.380000
 HB 4.293000
 CG2 22.670000
 HG2# 1.267000
 END_RES_DEF

RES_ID 756
 RES_TYPE GLU
 SPIN_SYSTEM_ID 42
 HETEROGENEITY 100

N 118.732000
 HN 7.209000
 CA 56.270000
 HA 4.448000
 CB 30.930000
 HB1 2.174000
 HB2 2.000000
 CG 36.440000
 HG1 2.292000
 END_RES_DEF

RES_ID 757
 RES_TYPE ALA
 SPIN_SYSTEM_ID 43
 HETEROGENEITY 100

N 122.504000
 HN 7.379000
 CA 50.220000
 HA 4.937000
 CB 19.370000
 HB# 1.082000
 END_RES_DEF

RES_ID 758
 RES_TYPE PRO
 SPIN_SYSTEM_ID 44
 HETEROGENEITY 100

CA 65.080000
 HA 4.496000
 CB 31.487000
 HB1 2.374000
 HB2 2.027000
 CG 27.632000
 HG1 2.122000
 HG2 2.038000
 CD 50.212000
 HD2 3.515000
 HD1 3.717000
 END_RES_DEF

RES_ID 759
 RES_TYPE GLY
 SPIN_SYSTEM_ID 45
 HETEROGENEITY 100
 END_RES_DEF

RES_ID 760
 RES_TYPE TYR
 SPIN_SYSTEM_ID 46
 HETEROGENEITY 100
 N 122.504000
 HN 7.945000
 CA 62.328000
 HA 3.536000

CB 39.750000
 HB1 2.689000
 HB2 2.487000
 CD1 133.799000
 HD1 5.120000
 CE1 118.379000
 HE1 6.070000
 END_RES_DEF

RES_ID 761
 RES_TYPE TYR
 SPIN_SYSTEM_ID 47
 HETEROGENEITY 100

N 113.157000
 HN 8.225000
 CA 60.676000
 HA 4.101000
 CB 37.550000
 HB1 3.189000
 HB2 2.801000
 CD1 134.901000
 HD1 7.342000
 CE1 118.930000
 HE1 6.646000
 END_RES_DEF

RES_ID 762
 RES_TYPE GLU
 SPIN_SYSTEM_ID 48
 HETEROGENEITY 100

N 117.912000
 HN 7.702000
 CA 57.922000
 HA 4.209000
 CB 29.480000
 HB1 2.086000
 CG 37.545000
 HG1 2.325000
 HG2 2.265000
 END_RES_DEF

RES_ID 763
 RES_TYPE VAL
 SPIN_SYSTEM_ID 49
 HETEROGENEITY 100

N 115.453000
 HN 7.135000
 CA 63.430000
 HA 4.077000
 CB 33.690000
 HB 2.015000
 CG1 21.020000
 HG1# 1.045000
 CG2 21.574000
 HG2# 0.991000
 END_RES_DEF

RES_ID 764
 RES_TYPE ILE
 SPIN_SYSTEM_ID 50
 HETEROGENEITY 100

N 122.832000
 HN 7.947000
 CA 57.920000
 HA 3.916000
 CB 34.240000
 HB 1.205000
 CG1 24.878000
 HG11 0.798000
 HG12 0.216000
 CG2 16.617000
 HG2# 0.380000
 CD1 9.457000
 HD1# 0.537000
 END_RES_DEF

RES_ID 765
 RES_TYPE ARG
 SPIN_SYSTEM_ID 51
 HETEROGENEITY 100

N 125.291000
 HN 7.749000
 CA 57.371000
 HA 3.875000
 CB 30.936000
 HB1 1.388000
 HB2 1.211000
 CG 27.080000
 HG1 1.319000
 HG2 1.173000
 CD 43.052000
 HD1 2.971000
 END_RES_DEF

RES_ID 766

HN 8.068000
CA 56.270000
HA 4.329000
CB 38.646000
HB1 2.877000
HB2 2.834000
END_RES_DEF

RES_ID 815
RES_TYPE ILE
SPIN_SYSTEM_ID 101
HETEROGENEITY 100
N 119.880000
HN 7.912000
CA 65.080000
HA 3.646000
CB 39.197000
HB 1.924000
CG1 29.284000
HG11 1.882000
HG12 1.201000
CG2 17.718000
HG2# 1.017000
CD1 13.863000
HD1# 0.940000
END_RES_DEF

RES_ID 816
RES_TYPE LEU
SPIN_SYSTEM_ID 102
HETEROGENEITY 100
N 122.504000
HN 8.556000
CA 56.820000
HA 3.670000
CB 41.951000
HB1 1.405000
HB2 1.199000
CG 26.530000
HG 1.580000
CD1 24.327000
HD1# 0.701000
CD2 25.429000
HD2# 0.696000
END_RES_DEF

RES_ID 817
RES_TYPE GLU
SPIN_SYSTEM_ID 103
HETEROGENEITY 100
N 120.700000
HN 8.073000
CA 60.125000
HA 3.185000
CB 29.835000
HB1 1.720000
HB2 1.310000
CG 37.545000
HG1 2.001000
HG2 1.922000
END_RES_DEF

RES_ID 818
RES_TYPE LYS
SPIN_SYSTEM_ID 104
HETEROGENEITY 100
N 117.584000
HN 7.145000
CA 59.688000
HA 4.075000
CB 32.588000
HB1 1.929000
CG 25.644000
HG1 1.492000
CD 29.284000
HD1 1.681000
CE 41.963000
HE1 2.964000
END_RES_DEF

RES_ID 819
RES_TYPE PHE
SPIN_SYSTEM_ID 105
HETEROGENEITY 100
N 121.028000
HN 7.869000
CA 61.230000
HA 4.328000
CB 39.200000
HB1 3.133000
HB2 3.047000
CD1 133.800000
HD1 7.180000
END_RES_DEF

RES_ID 820
RES_TYPE PHE
SPIN_SYSTEM_ID 106
HETEROGENEITY 100
N 120.700000
HN 9.126000
CA 60.691000
HA 3.961000
CB 38.640000
HB1 3.289000
HB2 3.067000
CD1 133.248000
HD1 6.904000
CE1 132.698000
HE1 7.011000
END_RES_DEF

RES_ID 821
RES_TYPE PHE
SPIN_SYSTEM_ID 107
HETEROGENEITY 100
N 118.076000
HN 8.359000
CA 61.770000
HA 3.840000
CB 38.090000
HB1 3.064000
CD1 133.248000
HD1 7.175000
CE1 132.698000
HE1 7.294000
CZ 131.596000
HZ 7.430000
END_RES_DEF

RES_ID 822
RES_TYPE SER
SPIN_SYSTEM_ID 108
HETEROGENEITY 100
N 114.961000
HN 7.906000
CA 61.773000
HA 4.200000
CB 62.879000
HB1 4.007000
END_RES_DEF

RES_ID 823
RES_TYPE LYS
SPIN_SYSTEM_ID 109
HETEROGENEITY 100
N 120.864000
HN 7.938000
CA 56.820000
HA 4.008000
CB 31.487000
HB1 1.730000
HB2 1.567000
CG 23.226000
HG1 0.833000
CD 27.080000
HD1 1.403000
CE 42.501000
HE1 2.569000
HE2 2.422000
END_RES_DEF

RES_ID 824
RES_TYPE ILE
SPIN_SYSTEM_ID 110
HETEROGENEITY 100
N 116.928000
HN 8.101000
CA 64.530000
HA 3.818000
CB 36.990000
HB 1.746000
CG1 26.530000
HG11 1.140000
HG12 1.073000
CG2 18.820000
HG2# 0.654000
CD1 13.312000
HD1# 0.541000
END_RES_DEF

RES_ID 825
RES_TYPE LYS
SPIN_SYSTEM_ID 111
HETEROGENEITY 100
N 122.176000
HN 7.546000
CA 59.024000
HA 4.043000
CB 32.360000

HB1 1.879000
HB2 1.757000
CG 24.878000
HG1 1.390000
HG2 1.302000
CD 29.284000
HD1 1.633000
CE 41.400000
HE1 2.913000
END_RES_DEF

RES_ID 826
RES_TYPE GLU
SPIN_SYSTEM_ID 112
HETEROGENEITY 100
N 121.192000
HN 8.063000
CA 59.024000
HA 3.995000
CB 29.834000
HB1 2.058000
CG 36.050000
HG1 2.342000
HG2 2.205000
END_RES_DEF

RES_ID 827
RES_TYPE ALA
SPIN_SYSTEM_ID 113
HETEROGENEITY 100
N 117.748000
HN 7.620000
CA 52.410000
HA 4.291000
CB 19.920000
HB# 1.358000
END_RES_DEF

RES_ID 828
RES_TYPE GLY
SPIN_SYSTEM_ID 114
HETEROGENEITY 100
N 126.767000
HN 7.744000
CA 45.902000
HA1 4.019000
HA2 3.935000
END_RES_DEF

RES_ID 829
RES_TYPE LEU
SPIN_SYSTEM_ID 115
HETEROGENEITY 100
N 117.912000
HN 7.742000
CA 55.719000
HA 4.215000
CB 43.052000
HB1 1.562000
CG 27.632000
HG 1.536000
CD1 23.776000
HD1# 0.711000
END_RES_DEF

RES_ID 830
RES_TYPE ILE
SPIN_SYSTEM_ID 116
HETEROGENEITY 100
N 115.453000
HN 7.458000
CA 60.676000
HA 4.232000
CB 39.748000
HB 1.810000
CG1 27.080000
HG11 1.314000
HG12 0.918000
CG2 17.718000
HG2# 0.815000
CD1 13.312000
HD1# 0.794000
END_RES_DEF

RES_ID 831
RES_TYPE ASP
SPIN_SYSTEM_ID 117
HETEROGENEITY 100
N 123.488000
HN 8.270000
CA 54.620000
HA 4.571000
CB 41.400000
HB1 2.693000
HB2 2.540000

END_RES_DEF
RES_ID 832
RES_TYPE LYS
SPIN_SYSTEM_ID 118
HETEROGENEITY 100
N 125.450000
HN 7.774000
CA 57.720000
HA 4.082000
CB 33.410000
END_RES_DEF

Unambiguous NOE-derived Inter-proton Distance Restraints

ASST1 { 2141 } (((segid "BFD" and resid 99 and name HN)) (((segid "BFD" and resid 98 and name HN)) (((segid "BFD" and resid 86 and name HN)) 4 200 4 200 1 300 peak 2141 weight ASST1 { 13262 } (((segid "BFD" and resid 89 and name HD221)) (((segid "BFD" and resid 95 and name HE4)) (((segid "BFD" and resid 11261 weight 0 11000E+01 volume 0 3675E+02 ppm1 8 857 ppm2	7 704
ASST1 { 13271 } (((segid "BFD" and resid 89 and name HD21)) (((segid "BFD" and resid 95 and name HE4)) (((segid "BFD" and resid 11261 weight 0 11000E+01 volume 0 50220E+02 ppm1 8 416 ppm2	7 624
ASST1 { 8521 } (((segid "BFD" and resid 89 and name HD21)) (((segid "BFD" and resid 95 and name HE4)) (((segid "BFD" and resid 11271 weight 0 11000E+01 volume 0 43992E+02 ppm1 8 934 ppm2	7 624
ASST1 { 14401 } (((segid "BFD" and resid 46 and name HN)) (((segid "BFD" and resid 45 and name HD4)) (((segid "BFD" and resid 44 and name HN)) 3 500 3 100 2 000 peak 4521 weight 0 11000E+01 volume 0 10017E+03 ppm1 8 562 ppm2	7 960
ASST1 { 14402 } (((segid "BFD" and resid 87 and name HN)) (((segid "BFD" and resid 88 and name HN)) (((segid "BFD" and resid 89 and name HD1)) 3 400 1 800 peak 14401 weight 0 11000E+01 volume 0 7218E+02 ppm1 8 572 ppm2	5 332
OR { 14403 } (((segid "BFD" and resid 87 and name HN)) (((segid "BFD" and resid 88 and name HN)) (((segid "BFD" and resid 89 and name HD1)) 3 400 1 800 peak 14401 weight 0 11000E+01 volume 0 7218E+02 ppm1 8 572 ppm2	5 332
ASST1 { 15611 } (((segid "BFD" and resid 87 and name HN)) (((segid "BFD" and resid 88 and name HN)) (((segid "BFD" and resid 89 and name HD1)) 3 400 1 800 peak 15611 weight 0 11000E+01 volume 0 2344E+02 ppm1 11 082 ppm2	3 143
OR { 15612 } (((segid "BFD" and resid 87 and name HN)) (((segid "BFD" and resid 88 and name HN)) (((segid "BFD" and resid 89 and name HD1)) 3 400 1 800 peak 15611 weight 0 11000E+01 volume 0 2344E+02 ppm1 11 082 ppm2	3 143
ASST1 { 11 } (((segid "BFD" and resid 43 and name HN)) (((segid "BFD" and resid 44 and name HN)) (((segid "BFD" and resid 45 and name HD1)) 2 700 1 800 1 800 peak 11 weight 0 11000E+01 volume 0 5245E+03 ppm1 8 001 ppm2	5 544
ASST1 { 2401 } (((segid "BFD" and resid 43 and name HN)) (((segid "BFD" and resid 44 and name HN)) (((segid "BFD" and resid 45 and name HD1)) 2 400 1 400 1 400 peak 11 weight 0 11000E+01 volume 0 9342E+03 ppm1 8 001 ppm2	1 689
ASST1 { 2402 } (((segid "BFD" and resid 43 and name HN)) (((segid "BFD" and resid 44 and name HN)) (((segid "BFD" and resid 45 and name HD1)) 2 400 1 400 1 400 peak 21 weight 0 11000E+01 volume 0 18953E+04 ppm1 8 001 ppm2	7 816
ASST1 { 31 } (((segid "BFD" and resid 42 and name HN)) (((segid "BFD" and resid 41 and name HB)) (((segid "BFD" and resid 40 and name HB)) 2 300 2 700 2 400 peak 31 weight 0 11000E+01 volume 0 14380E+03 ppm1 7 822 ppm2	4 900
ASST1 { 41 } (((segid "BFD" and resid 42 and name HN)) (((segid "BFD" and resid 41 and name HB)) (((segid "BFD" and resid 40 and name HB)) 2 300 2 700 2 400 peak 41 weight 0 11000E+01 volume 0 30790E+03 ppm1 7 824 ppm2	5 053
ASST1 { 51 } (((segid "BFD" and resid 42 and name HN)) (((segid "BFD" and resid 41 and name HB)) (((segid "BFD" and resid 40 and name HB)) 2 700 1 800 1 800 peak 51 weight 0 11000E+01 volume 0 4734E+03 ppm1 7 821 ppm2	2 613
ASST1 { 61 } (((segid "BFD" and resid 42 and name HN)) (((segid "BFD" and resid 41 and name HB)) (((segid "BFD" and resid 40 and name HB)) 2 700 2 600 2 300 peak 61 weight 0 11000E+01 volume 0 16643E+03 ppm1 7 822 ppm2	2 899
ASST1 { 71 } (((segid "BFD" and resid 42 and name HN)) (((segid "BFD" and resid 41 and name HB)) (((segid "BFD" and resid 40 and name HB)) 3 400 2 900 2 100 peak 71 weight 0 11000E+01 volume 0 13090E+03 ppm1 7 821 ppm2	2 790
ASST1 { 91 } (((segid "BFD" and resid 42 and name HN)) (((segid "BFD" and resid 41 and name HB)) (((segid "BFD" and resid 40 and name HB)) 2 400 1 400 1 400 peak 91 weight 0 11000E+01 volume 0 9667E+03 ppm1 8 936 ppm2	2 208
ASST1 { 101 } (((segid "BFD" and resid 99 and name HN)) (((segid "BFD" and resid 98 and name HN)) (((segid "BFD" and resid 97 and name HN)) 2 800 1 800 1 800 peak 101 weight 0 11000E+01 volume 0 42952E+03 ppm1 8 936 ppm2	4 441
ASST1 { 121 } (((segid "BFD" and resid 99 and name HN)) (((segid "BFD" and resid 98 and name HN)) (((segid "BFD" and resid 97 and name HN)) 2 700 1 800 1 800 peak 121 weight 0 11000E+01 volume 0 45504E+03 ppm1 8 936 ppm2	9 112
SSI { 131 } (((segid "BFD" and resid 98 and name HN)) (((segid "BFD" and resid 97 and name HA)) (((segid "BFD" and resid 96 and name HA)) 2 500 1 600 1 600 peak 131 weight 0 11000E+01 volume 0 72592E+03 ppm1 9 125 ppm2	4 811
ASST1 { 141 } (((segid "BFD" and resid 98 and name HN)) (((segid "BFD" and resid 97 and name HN)) (((segid "BFD" and resid 96 and name HN)) 3 300 2 700 2 200 peak 141 weight 0 11000E+01 volume 0 15487E+03 ppm1 9 125 ppm2	4 010

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(( segid "BPD " and read1 106 and name H82 ))
ASSI { 451 }
2 300 1 300 1 300 peak 431 weight
(( segid "BPD " and read1 107 and name H81 ))
(( segid "BPD " and read1 106 and name H81 ))
ASSI { 461 }
2 100 2 100 peak 451 weight
0 11000E+01 volume 0.11998E+04 ppm1
(( segid "BPD " and read1 107 and name H81 ))
(( segid "BPD " and read1 106 and name H81 ))
ASSI { 471 }
3 100 3 100 2 000 peak 461 weight
0 11000E+01 volume 0.11258E+03 ppm1
(( segid "BPD " and read1 107 and name H81 ))
(( segid "BPD " and read1 106 and name H81 ))
ASSI { 481 }
2 600 1 700 1 700 peak 471 weight
0 11000E+01 volume 0.57631E+03 ppm1
(( segid "BPD " and read1 107 and name H81 ))
(( segid "BPD " and read1 106 and name H81 ))
ASSI { 491 }
2 600 2 600 2 300 peak 481 weight
0 11000E+01 volume 0.16715E+03 ppm1
(( segid "BPD " and read1 106 and name H81 ))
(( segid "BPD " and read1 107 and name H81 ))
ASSI { 501 }
2 600 1 700 1 700 peak 501 weight
0 11000E+01 volume 0.57311E+03 ppm1
(( segid "BPD " and read1 106 and name H81 ))
(( segid "BPD " and read1 107 and name H81 ))
ASSI { 511 }
2 700 1 800 1 800 peak 511 weight
0 11000E+01 volume 0.52916E+03 ppm1
(( segid "BPD " and read1 106 and name H81 ))
(( segid "BPD " and read1 107 and name H81 ))
ASSI { 521 }
1 400 1 400 peak 521 weight
0 11000E+01 volume 0.97994E+03 ppm1
(( segid "BPD " and read1 106 and name H81 ))
(( segid "BPD " and read1 107 and name H81 ))
ASSI { 531 }
2 300 1 300 1 300 peak 531 weight
0 11000E+01 volume 0.11922E+04 ppm1
(( segid "BPD " and read1 106 and name H81 ))
(( segid "BPD " and read1 107 and name H81 ))
ASSI { 541 }
2 900 2 400 2 100 peak 541 weight
0 11000E+01 volume 0.32815E+03 ppm1
(( segid "BPD " and read1 110 and name H81 ))
(( segid "BPD " and read1 110 and name H81 ))
ASSI { 551 }
2 000 2 000 peak 551 weight
0 11000E+01 volume 0.44829E+03 ppm1
(( segid "BPD " and read1 111 and name H81 ))
(( segid "BPD " and read1 111 and name H81 ))
ASSI { 561 }
2 000 2 000 peak 561 weight
0 11000E+01 volume 0.17650E+03 ppm1
(( segid "BPD " and read1 111 and name H81 ))
(( segid "BPD " and read1 111 and name H81 ))
ASSI { 571 }
2 500 1 600 1 600 peak 561 weight
0 11000E+01 volume 0.71549E+03 ppm1
(( segid "BPD " and read1 110 and name H81 ))
(( segid "BPD " and read1 111 and name H81 ))
ASSI { 581 }
2 800 2 000 2 000 peak 571 weight
0 11000E+01 volume 0.38661E+03 ppm1
(( segid "BPD " and read1 112 and name H81 ))
(( segid "BPD " and read1 112 and name H81 ))
ASSI { 591 }
2 200 1 300 1 300 peak 581 weight
0 11000E+01 volume 0.13944E+04 ppm1
(( segid "BPD " and read1 112 and name H81 ))
(( segid "BPD " and read1 112 and name H81 ))
ASSI { 601 }
3 400 2 900 2 100 peak 591 weight
0 11000E+01 volume 0.12114E+03 ppm1
(( segid "BPD " and read1 112 and name H81 ))
(( segid "BPD " and read1 112 and name H81 ))
ASSI { 611 }
3 100 2 000 peak 601 weight
0 11000E+01 volume 0.96211E+02 ppm1
(( segid "BPD " and read1 112 and name H81 ))
(( segid "BPD " and read1 112 and name H81 ))
ASSI { 621 }
2 200 1 200 1 200 peak 611 weight
0 11000E+01 volume 0.15417E+04 ppm1
(( segid "BPD " and read1 113 and name H81 ))
(( segid "BPD " and read1 113 and name H81 ))
ASSI { 631 }
2 800 2 000 2 000 peak 621 weight
0 11000E+01 volume 0.42878E+03 ppm1
(( segid "BPD " and read1 113 and name H81 ))
(( segid "BPD " and read1 113 and name H81 ))
ASSI { 641 }
2 800 2 000 2 000 peak 631 weight
0 11000E+01 volume 0.99017E+03 ppm1
(( segid "BPD " and read1 114 and name H81 ))
(( segid "BPD " and read1 114 and name H81 ))
ASSI { 651 }
2 800 2 000 2 000 peak 641 weight
0 11000E+01 volume 0.42782E+03 ppm1
(( segid "BPD " and read1 113 and name H81 ))
(( segid "BPD " and read1 113 and name H81 ))
ASSI { 661 }
2 500 1 600 1 600 peak 651 weight
0 11000E+01 volume 0.73856E+03 ppm1

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[illegible]

(((egid "BTD" * and read 78 * and name HA))	3 300	2 700	2 200 peak 5031 weight	0 11000E+01 volume	0 14659E+03 ppm1	8 681 ppm2	3 995	
ASST { 5041 }								
(((egid "BTD" * and read 78 * and name HN))	3 400	2 900	2 100 peak 5301 weight	0 11000E+01 volume	0 12542E+03 ppm1	8 858 ppm2	4 978	
ASST { 5041 }								
(((egid "BTD" * and read 79 * and name HA))	3 400	2 900	2 100 peak 5301 weight	0 11000E+01 volume	0 14043E+04 ppm1	7 996 ppm2	8 687	
ASST { 5061 }								
(((egid "BTD" * and read 80 * and name HN))	5 300	5 300	0 200 peak 5061 weight	0 11000E+01 volume	0 85899E+01 ppm1	8 006 ppm2	3 997	
ASST { 5061 }								
(((egid "BTD" * and read 80 * and name HD1))	3 300	2 700	2 200 peak 5071 weight	0 11000E+01 volume	0 15955E+03 ppm1	8 006 ppm2	4 404	
ASST { 5091 }								
(((egid "BTD" * and read 80 * and name HN))	3 300	2 700	2 200 peak 5071 weight	0 11000E+01 volume	0 14421E+03 ppm1	8 006 ppm2	2 704	
ASST { 5101 }								
(((egid "BTD" * and read 81 * and name HA))	3 300	2 700	2 200 peak 5101 weight	0 11000E+01 volume	0 77456E+02 ppm1	7 439 ppm2	4 685	
ASST { 5101 }								
(((egid "BTD" * and read 81 * and name HN))	3 400	3 400	1 600 peak 5101 weight	0 11000E+01 volume	0 81862E+03 ppm1	6 981 ppm2	2 042	
ASST { 5111 }								
(((egid "BTD" * and read 81 * and name HB))	2 500	1 600	1 600 peak 5111 weight	0 11000E+01 volume	0 17052E+03 ppm1	6 981 ppm2	1 086	
ASST { 5121 }								
(((egid "BTD" * and read 82 * and name HN))	3 200	2 400	2 300 peak 5121 weight	0 11000E+01 volume	0 17068E+03 ppm1	6 981 ppm2	0 749	
ASST { 5131 }								
(((egid "BTD" * and read 82 * and name HN))	3 400	3 400	2 100 peak 5131 weight	0 11000E+01 volume	0 13164E+03 ppm1	9 658 ppm2	4 743	
ASST { 5141 }								
(((egid "BTD" * and read 82 * and name HA))	3 400	2 900	2 100 peak 5141 weight	0 11000E+01 volume	0 10793E+03 ppm1	9 660 ppm2	3 697	
ASST { 5151 }								
(((egid "BTD" * and read 83 * and name HN))	3 500	3 100	2 000 peak 5151 weight	0 11000E+01 volume	0 10793E+03 ppm1	9 660 ppm2	3 551	
ASST { 5161 }								
(((egid "BTD" * and read 83 * and name HN))	3 200	2 400	2 000 peak 5161 weight	0 11000E+01 volume	0 41394E+03 ppm1	9 658 ppm2	4 817	
ASST { 5171 }								
(((egid "BTD" * and read 84 * and name HN))	3 200	2 600	2 300 peak 5171 weight	0 11000E+01 volume	0 19068E+03 ppm1	9 466 ppm2	4 449	
ASST { 5181 }								
(((egid "BTD" * and read 84 * and name HA))	3 600	3 200	1 900 peak 5181 weight	0 11000E+01 volume	0 83498E+02 ppm1	9 463 ppm2	1 903	
ASST { 5191 }								
(((egid "BTD" * and read 84 * and name HN))	3 500	3 100	2 000 peak 5191 weight	0 11000E+01 volume	0 11050E+03 ppm1	9 463 ppm2	7 515 ppm2	3 268
ASST { 5201 }								
(((egid "BTD" * and read 85 * and name HN))	3 400	3 400	1 600 peak 5201 weight	0 11000E+01 volume	0 79848E+02 ppm1	8 423 ppm2	5 012	
ASST { 5211 }								
(((egid "BTD" * and read 85 * and name HN))	3 400	2 900	2 100 peak 5211 weight	0 11000E+01 volume	0 12439E+03 ppm1	7 516 ppm2	3 639	
ASST { 5221 }								
(((egid "BTD" * and read 85 * and name HN))	3 300	3 300	1 600 peak 5221 weight	0 11000E+01 volume	0 50221E+02 ppm1	8 423 ppm2	4 857	
ASST { 5231 }								
(((egid "BTD" * and read 86 * and name HN))	3 400	3 400	2 200 peak 5231 weight	0 11000E+01 volume	0 14503E+03 ppm1	8 423 ppm2	4 815	
ASST { 5241 }								
(((egid "BTD" * and read 87 * and name HA))	3 600	3 200	1 900 peak 5241 weight	0 11000E+01 volume	0 84948E+02 ppm1	8 572 ppm2	2 762	
ASST { 5251 }								
(((egid "BTD" * and read 88 * and name HN))	3 400	3 200	1 900 peak 5251 weight	0 11000E+01 volume	0 87457E+02 ppm1	8 357 ppm2	8 354 ppm2	2 614
ASST { 5261 }								
(((egid "BTD" * and read 88 * and name HN))	3 200	2 400	2 300 peak 5271 weight	0 11000E+01 volume	0 19424E+03 ppm1	8 354 ppm2	8 552	
ASST { 5271 }								
(((egid "BTD" * and read 88 * and name HB))	2 600	1 700	1 700 peak 5281 weight	0 11000E+01 volume	0 67695E+03 ppm1	8 355 ppm2		
ASST { 5281 }								
(((egid "BTD" * and read 88 * and name HN))	3 200	2 400	2 300 peak 5271 weight	0 11000E+01 volume	0 17139E+03 ppm1	8 674 ppm2	3 997	
ASST { 5291 }								
(((egid "BTD" * and read 88 * and name HN))	2 600	1 700	1 700 peak 5281 weight	0 11000E+01 volume	0 16985E+03 ppm1	8 936 ppm2	4 813	
ASST { 5301 }								
(((egid "BTD" * and read 89 * and name HN))	3 400	2 900	2 100 peak 5301 weight	0 11000E+01 volume	0 12542E+03 ppm1	8 858 ppm2	4 978	
ASST { 5311 }								
(((egid "BTD" * and read 89 * and name HN))	3 400	2 900	2 100 peak 5301 weight	0 11000E+01 volume	0 14043E+04 ppm1	7 996 ppm2	8 687	
ASST { 5361 }								
(((egid "BTD" * and read 89 * and name HD1))	5 300	5 300	0 200 peak 5061 weight	0 11000E+01 volume	0 85899E+01 ppm1	8 006 ppm2	3 997	
ASST { 5361 }								
(((egid "BTD" * and read 89 * and name HN))	3 300	2 700	2 200 peak 5071 weight	0 11000E+01 volume	0 15955E+03 ppm1	8 006 ppm2	4 404	
ASST { 5391 }								
(((egid "BTD" * and read 89 * and name HN))	3 300	2 700	2 200 peak 5071 weight	0 11000E+01 volume	0 14421E+03 ppm1	8 006 ppm2	2 704	
ASST { 5401 }								
(((egid "BTD" * and read 90 * and name HA))	3 300	2 700	2 200 peak 5101 weight	0 11000E+01 volume	0 77456E+02 ppm1	7 439 ppm2	4 685	
ASST { 5401 }								
(((egid "BTD" * and read 90 * and name HN))	3 400	3 400	1 600 peak 5101 weight	0 11000E+01 volume	0 81862E+03 ppm1	6 981 ppm2	2 042	
ASST { 5411 }								
(((egid "BTD" * and read 90 * and name HB))	2 500	1 600	1 600 peak 5111 weight	0 11000E+01 volume	0 17052E+03 ppm1	6 981 ppm2	1 086	
ASST { 5421 }								
(((egid "BTD" * and read 91 * and name HN))	3 200	2 400	2 300 peak 5121 weight	0 11000E+01 volume	0 17068E+03 ppm1	6 981 ppm2	0 749	
ASST { 5431 }								
(((egid "BTD" * and read 91 * and name HN))	3 400	3 400	2 100 peak 5131 weight	0 11000E+01 volume	0 13164E+03 ppm1	9 658 ppm2	4 743	
ASST { 5441 }								
(((egid "BTD" * and read 91 * and name HA))	3 400	2 900	2 100 peak 5141 weight	0 11000E+01 volume	0 10793E+03 ppm1	9 660 ppm2	3 697	
ASST { 5451 }								
(((egid "BTD" * and read 92 * and name HN))	3 500	3 100	2 000 peak 5151 weight	0 11000E+01 volume	0 10793E+03 ppm1	9 660 ppm2	3 551	
ASST { 5461 }								
(((egid "BTD" * and read 92 * and name HN))	3 200	2 400	2 000 peak 5161 weight	0 11000E+01 volume	0 41394E+03 ppm1	9 658 ppm2	4 817	
ASST { 5471 }								
(((egid "BTD" * and read 92 * and name HN))	3 200	2 600	2 300 peak 5171 weight	0 11000E+01 volume	0 19068E+03 ppm1	9 466 ppm2	4 449	
ASST { 5481 }								
(((egid "BTD" * and read 93 * and name HA))	3 600	3 200	1 900 peak 5181 weight	0 11000E+01 volume	0 83498E+02 ppm1	9 463 ppm2	1 903	
ASST { 5491 }								
(((egid "BTD" * and read 93 * and name HN))	3 500	3 100	2 000 peak 5191 weight	0 11000E+01 volume	0 11050E+03 ppm1	9 463 ppm2	7 515 ppm2	3 268
ASST { 5501 }								
(((egid "BTD" * and read 94 * and name HN))	3 400	3 400	1 600 peak 5201 weight	0 11000E+01 volume	0 79848E+02 ppm1	8 423 ppm2	5 012	
ASST { 5511 }								
(((egid "BTD" * and read 94 * and name HN))	3 400	2 900	2 100 peak 5211 weight	0 11000E+01 volume	0 12439E+03 ppm1	7 516 ppm2	3 639	
ASST { 5521 }								
(((egid "BTD" * and read 95 * and name HN))	3 300	3 300	1 600 peak 5221 weight	0 11000E+01 volume	0 50221E+02 ppm1	8 423 ppm2	4 857	
ASST { 5531 }								
(((egid "BTD" * and read 95 * and name HN))	3 400	3 400	2 200 peak 5231 weight	0 11000E+01 volume	0 14503E+03 ppm1	8 423 ppm2	4 815	
ASST { 5541 }								
(((egid "BTD" * and read 96 * and name HA))	3 600	3 200	1 900 peak 5241 weight	0 11000E+01 volume	0 84948E+02 ppm1	8 572 ppm2	2 762	
ASST { 5551 }								
(((egid "BTD" * and read 96 * and name HN))	3 400	3 200	1 900 peak 5251 weight	0 11000E+01 volume	0 87457E+02 ppm1	8 357 ppm2	8 354 ppm2	2 614
ASST { 5561 }								
(((egid "BTD" * and read 97 * and name HN))	3 200	2 400	2 300 peak 5271 weight	0 11000E+01 volume	0 19424E+03 ppm1	8 354 ppm2	8 552	
ASST { 5571 }								
(((egid "BTD" * and read 97 * and name HB))	2 600	1 700	1 700 peak 5281 weight	0 11000E+01 volume	0 67695E+03 ppm1	8 355 ppm2		
ASST { 5581 }								
(((egid "BTD" * and read 97 * and name HN))	3 200	2 400	2 300 peak 5271 weight	0 11000E+01 volume	0 17139E+03 ppm1	8 674 ppm2	3 997	
ASST { 5591 }								
(((egid "BTD" * and read 98 * and name HN))	2 600	1 700	1 700 peak 5281 weight	0 11000E+01 volume	0 16985E+03 ppm1	8 936 ppm2	4 813	
ASST { 5601 }								
(((egid "BTD" * and read 98 * and name HN))	3 400	2 900	2 100 peak 5301 weight	0 11000E+01 volume	0 12542E+03 ppm1	8 858 ppm2	4 978	
ASST { 5611 }								
(((egid "BTD" * and read 98 * and name HN))	3 400	2 900	2 100 peak 5301 weight	0 11000E+01 volume	0 14043E+04 ppm1	7 996 ppm2	8 687	
ASST { 5661 }								
(((egid "BTD" * and read 98 * and name HD1))	5 300	5 300	0 200 peak 5061 weight	0 11000E+01 volume	0 85899E+01 ppm1	8 006 ppm2	3 997	
ASST { 5661 }								
(((egid "BTD" * and read 98 * and name HN))	3 300	2 700	2 200 peak 5071 weight	0 11000E+01 volume	0 15955E+03 ppm1	8 006 ppm2	4 404	
ASST { 5691 }								
(((egid "BTD" * and read 98 * and name HN))	3 300	2 700	2 200 peak 5071 weight	0 11000E+01 volume	0 14421E+03 ppm1	8 006 ppm2	2 704	
ASST { 5701 }								
(((egid "BTD" * and read 99 * and name HA))	3 300	2 700	2 200 peak 5101 weight	0 11000E+01 volume	0 77456E+02 ppm1	7 439 ppm2	4 685	
ASST { 5701 }								
(((egid "BTD" * and read 99 * and name HN))	3 400	3 400	1 600 peak 5101 weight	0 11000E+01 volume	0 81862E+03 ppm1	6 981 ppm2	2 042	
ASST { 5711 }								
(((egid "BTD" * and read 99 * and name HB))	2 500	1 600	1 600 peak 5111 weight	0 11000E+01 volume	0 17052E+03 ppm1	6 981 ppm2	1 086	
ASST { 5721 }								
(((egid "BTD" * and read 99 * and name HN))	3 200	2 400	2 300 peak 5121 weight	0 11000E+01 volume	0 17068E+03 ppm1	6 981 ppm2	0 749	
ASST { 5731 }								
(((egid "BTD" * and read 99 * and name HN))	3 400	3 400	2 100 peak 5131 weight	0 11000E+01 volume	0 13164E+03 ppm1	9 658 ppm2	4 743	
ASST { 5741 }								
(((egid "BTD" * and read 99 * and name HA))	3 400	2 900	2 100 peak 5141 weight	0 11000E+01 volume	0 10793E+03 ppm1	9 660 ppm2	3 697	
ASST { 5751 }								
(((egid "BTD" * and read 99 * and name HN))	3 500	3 100	2 000 peak 5151 weight	0 11000E+01 volume	0 10793E+03 ppm1	9 660 ppm2	3 551	
ASST { 5761 }								
(((egid "BTD" * and read 99 * and name HN))	3 200	2 400	2 000 peak 5161 weight	0 11000E+01 volume	0 41394E+03 ppm1	9 658 ppm2	4 817	
ASST { 5771 }								
(((egid "BTD" * and read 99 * and name HN))	3 200	2 600	2 300 peak 5171 weight	0 11000E+01 volume	0 19068E+03 ppm1	9 466 ppm2	4 449	
ASST { 5781 }								
(((egid "BTD" * and read 99 * and name HA))	3 600	3 200	1 900 peak 5181 weight	0 11000E+01 volume	0 83498E+02 ppm1	9 463 ppm2	1 903	
ASST { 5791 }								
(((egid "BTD" * and read 99 * and name HN))	3 500	3 100	2 000 peak 5191 weight	0 11000E+01 volume	0 11050E+03 ppm1	9 463 ppm2	7 515 ppm2	3 268
ASST { 5801 }								
(((egid "BTD" * and read 99 * and name HN))	3 400	3 400	1 600 peak 5201 weight	0 11000E+01 volume	0 79848E+02 ppm1	8 423 ppm2	5 012	
ASST { 5811 }								
(((egid "BTD" * and read 99 * and name HN))	3 400	2 900	2 100 peak 5211 weight	0 11000E+01 volume	0 12439E+03 ppm1	7 516 ppm2	3 639	
ASST { 5821 }								
(((egid "BTD" * and read 99 * and name HN))	3 300	3 300	1 600 peak 5221 weight	0 11000E+01 volume	0 50221E+02 ppm1	8 423 ppm2	4 857	
ASST { 5831 }								
(((egid "BTD" * and read 99 * and name HN))	3 400	3 400	2 200 peak 5231 weight	0 11000E+01 volume	0 14503E+03 ppm1	8 423 ppm2	4 815	
ASST { 5841 }								
(((egid "BTD" * and read 99 * and name HN))	3 600	3 200	1 900 peak 5241 weight	0 11000E+01 volume	0 84948E+02 ppm1	8 572 ppm2	2 762	
ASST { 5851 }								
(((egid "BTD" * and read 99 * and name HN))	3 400	3 200						

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((segid "BTD" " and readid 28 and name HB3))	4.400	4.400	1.100 peak 11391 weight	0.10000E+01 volume	0.26154E+02 ppm1	12.276 ppm2	3.392
ASSI [11201]							
((segid "BTD" " and readid 30 and name HN))							
((segid "BTD" " and readid 28 and name HB1))							
ASSI [12093]	4.000	1.500 peak 12061 weight	0.10000E+01 volume	0.47923E+02 ppm1	8.669 ppm2	4.255	
ASSI [12111]							
((segid "BTD" " and readid 30 and name HN))							
((segid "BTD" " and readid 32 and name HN))							
ASSI [11141]	3.600	3.200	1.900 peak 11211 weight	0.10000E+01 volume	0.82028E+02 ppm1	12.276 ppm2	7.741
ASSI [11142]							
((segid "BTD" " and readid 31 and name HN))							
((segid "BTD" " and readid 28 and name HB1))							
ASSI [11251]	3.600	3.200	1.900 peak 11241 weight	0.10000E+01 volume	0.94605E+02 ppm1	8.480 ppm2	3.594
ASSI [11252]							
((segid "BTD" " and readid 31 and name HN))							
((segid "BTD" " and readid 28 and name HB2))							
ASSI [11361]	3.600	1.700 peak 11251 weight	0.10000E+01 volume	0.64760E+02 ppm1	8.481 ppm2	3.389	
ASSI [11362]							
((segid "BTD" " and readid 32 and name HN))							
((segid "BTD" " and readid 102 and name HB4))							
ASSI [11391]	4.500	4.500	1.000 peak 11361 weight	0.10000E+01 volume	0.23592E+02 ppm1	7.738 ppm2	1.310
ASSI [11392]							
((segid "BTD" " and readid 34 and name HN))							
((segid "BTD" " and readid 35 and name HB1))							
ASSI [11431]	3.200	2.600	2.300 peak 11391 weight	0.10000E+01 volume	0.18511E+03 ppm1	8.182 ppm2	3.447
ASSI [11432]							
((segid "BTD" " and readid 34 and name HN))							
((segid "BTD" " and readid 31 and name HB1))							
ASSI [11441]	2.100	2.100 peak 11431 weight	0.10000E+01 volume	0.29794E+03 ppm1	8.179 ppm2	2.301	
ASSI [11442]							
((segid "BTD" " and readid 34 and name HN))							
((segid "BTD" " and readid 56 and name HB1))							
ASSI [11451]	3.400	2.900	2.100 peak 11441 weight	0.10000E+01 volume	0.13941E+03 ppm1	8.184 ppm2	1.527
ASSI [11452]							
((segid "BTD" " and readid 34 and name HN))							
((segid "BTD" " and readid 102 and name HB1))							
ASSI [11521]	3.600	3.200	1.900 peak 11451 weight	0.10000E+01 volume	0.84106E+02 ppm1	8.185 ppm2	1.305
ASSI [11522]							
((segid "BTD" " and readid 35 and name HN))							
((segid "BTD" " and readid 56 and name HB1))							
ASSI [11561]	4.300	1.900 peak 11521 weight	0.10000E+01 volume	0.22012E+02 ppm1	7.734 ppm2	1.553	
ASSI [11562]							
((segid "BTD" " and readid 36 and name HN))							
((segid "BTD" " and readid 57 and name HB1))							
ASSI [11571]	3.400	2.900	2.100 peak 11561 weight	0.10000E+01 volume	0.11642E+03 ppm1	8.308 ppm2	2.953
ASSI [11572]							
((segid "BTD" " and readid 66 and name HN))							
((segid "BTD" " and readid 61 and name HB1))							
ASSI [11601]	4.200	4.200	1.300 peak 11571 weight	0.10000E+01 volume	0.34773E+02 ppm1	8.763 ppm2	1.640
ASSI [11602]							
((segid "BTD" " and readid 67 and name HN))							
((segid "BTD" " and readid 68 and name HB1))							
ASSI [11651]	4.400	1.400 peak 11601 weight	0.10000E+01 volume	0.26280E+02 ppm1	8.832 ppm2	7.780	
ASSI [11652]							
((segid "BTD" " and readid 68 and name HN))							
((segid "BTD" " and readid 69 and name HB1))							
ASSI [11661]	3.700	3.400	1.800 peak 11651 weight	0.10000E+01 volume	0.74566E+02 ppm1	8.626 ppm2	2.947
ASSI [11662]							
((segid "BTD" " and readid 68 and name HN))							
((segid "BTD" " and readid 38 and name HB1))							
ASSI [11731]	5.900	5.500	0.000 peak 11661 weight	0.10000E+01 volume	0.40913E+01 ppm1	8.426 ppm2	1.050
ASSI [11732]							
((segid "BTD" " and readid 70 and name HN))							
((segid "BTD" " and readid 68 and name HB1))							
ASSI [11741]	3.200	1.900 peak 11731 weight	0.10000E+01 volume	0.91804E+02 ppm1	8.040 ppm2	3.689	
ASSI [11742]							
((segid "BTD" " and readid 70 and name HN))							
((segid "BTD" " and readid 74 and name HB1))							
ASSI [11771]	3.400	2.900	2.100 peak 11741 weight	0.10000E+01 volume	0.13333E+03 ppm1	8.039 ppm2	3.544
ASSI [11772]							
((segid "BTD" " and readid 70 and name HN))							
((segid "BTD" " and readid 76 and name HB1))							
ASSI [11841]	3.700	3.400	2.800 peak 11771 weight	0.10000E+01 volume	0.79556E+02 ppm1	8.040 ppm2	2.491
ASSI [11842]							
((segid "BTD" " and readid 71 and name HN))							
((segid "BTD" " and readid 70 and name HB2))							
ASSI [12111]	2.600	2.300 peak 11841 weight	0.10000E+01 volume	0.16893E+03 ppm1	8.047 ppm2	4.361	
ASSI [12112]							
((segid "BTD" " and readid 74 and name HN))							
((segid "BTD" " and readid 75 and name HB2))							
ASSI [11911]	4.700	4.700	0.800 peak 11891 weight	0.10000E+01 volume	0.18157E+02 ppm1	7.534 ppm2	2.088
ASSI [11912]							
((segid "BTD" " and readid 74 and name HN))							
((segid "BTD" " and readid 76 and name HB1))							
ASSI [12031]	4.400	4.400	1.100 peak 11911 weight	0.10000E+01 volume	0.27875E+02 ppm1	7.534 ppm2	2.088
ASSI [12032]							
((segid "BTD" " and readid 99 and name HN))							
((segid "BTD" " and readid 100 and name HB2))							
ASSI [12061]	3.800	3.600	1.700 peak 12031 weight	0.10000E+01 volume	0.61445E+02 ppm1	8.934 ppm2	3.439
ASSI [12062]							
((segid "BTD" " and readid 99 and name HN))							
((segid "BTD" " and readid 97 and name HB1))							
ASSI [12751]	3.400	2.900	2.100 peak 12041 weight	0.10000E+01 volume	0.12562E+03 ppm1	8.934 ppm2	2.721
ASSI [12752]							
((segid "BTD" " and readid 100 and name HN))							
((segid "BTD" " and readid 101 and name HB1))							
ASSI [12761]	3.600	3.200	1.900 peak 12621 weight	0.10000E+01 volume	0.90949E+02 ppm1	7.762 ppm2	1.797
ASSI [12762]							
((segid "BTD" " and readid 52 and name HN))							
((segid "BTD" " and readid 53 and name HB1))							
ASSI [12771]	3.800	1.600 peak 12701 weight	0.10000E+01 volume	0.53690E+02 ppm1	9.004 ppm2	2.820	
ASSI [12772]							
((segid "BTD" " and readid 52 and name HN))							
((segid "BTD" " and readid 53 and name HB1))							
ASSI [12781]	3.100	2.400	2.400 peak 12741 weight	0.10000E+01 volume	0.21409E+03 ppm1	7.820 ppm2	2.491
ASSI [12782]							
((segid "BTD" " and readid 42 and name HN))							
((segid "BTD" " and readid 43 and name HB1))							
ASSI [12791]	3.100	2.400	2.400 peak 12741 weight	0.10000E+01 volume	0.21409E+03 ppm1	7.820 ppm2	2.491
ASSI [12792]							
((segid "BTD" " and readid 42 and name HN))							
((segid "BTD" " and readid 43 and name HB1))							
ASSI [12801]	3.100	2.400	2.400 peak 12741 weight	0.10000E+01 volume	0.21409E+03 ppm1	7.820 ppm2	2.491
ASSI [12802]							
((segid "BTD" " and readid 42 and name HN))							
((segid "BTD" " and readid 43 and name HB1))							
ASSI [12811]	3.100	2.400	2.400 peak 12741 weight	0.10000E+01 volume	0.21409E+03 ppm1	7.820 ppm2	2.491
ASSI [12812]							
((segid "BTD" " and readid 42 and name HN))							
((segid "BTD" " and readid 43 and name HB1))							
ASSI [12821]	3.100	2.400	2.400 peak 12741 weight	0.10000E+01 volume	0.21409E+03 ppm1	7.820 ppm2	2.491
ASSI [12822]							
((segid "BTD" " and readid 42 and name HN))							
((segid "BTD" " and readid 43 and name HB1))							
ASSI [12831]	3.100	2.400	2.400 peak 12741 weight	0.10000E+01 volume	0.21409E+03 ppm1	7.820 ppm2	2.491
ASSI [12832]							
((segid "BTD" " and readid 42 and name HN))							
((segid "BTD" " and readid 43 and name HB1))							
ASSI [12841]	3.100	2.400	2.400 peak 12741 weight	0.10000E+01 volume	0.21409E+03 ppm1	7.820 ppm2	2.491
ASSI [12842]							
((segid "BTD" " and readid 42 and name HN))							
((segid "BTD" " and readid 43 and name HB1))							
ASSI [12851]	3.100	2.400	2.400 peak 12741 weight	0.10000E+01 volume	0.21409E+03 ppm1	7.820 ppm2	2.491
ASSI [12852]							
((segid "BTD" " and readid 42 and name HN))							
((segid "BTD" " and readid 43 and name HB1))							
ASSI [12861]	3.100	2.400	2.400 peak 12741 weight	0.10000E+01 volume	0.21409E+03 ppm1	7.820 ppm2	2.491
ASSI [12862]							
((segid "BTD" " and readid 42 and name HN))							
((segid "BTD" " and readid 43 and name HB1))							
ASSI [12871]	3.100	2.400	2.400 peak 12741 weight	0.10000E+01 volume	0.21409E+03 ppm1	7.820 ppm2	2.491
ASSI [12872]							
((segid "BTD" " and readid 42 and name HN))							
((segid "BTD" " and readid 43 and name HB1))							
ASSI [12881]	3.100	2.400	2.400 peak 12741 weight	0.10000E+01 volume	0.21409E+03 ppm1	7.820 ppm2	2.491
ASSI [12882]							
((segid "BTD" " and readid 42 and name HN))							
((segid "BTD" " and readid 43 and name HB1))							
ASSI [12891]	3.100	2.400	2.400 peak 12741 weight	0.10000E+01 volume	0.21409E+03 ppm1	7.820 ppm2	2.491
ASSI [12892]							
((segid "BTD" " and readid 42 and name HN))							
((segid "BTD" " and readid 43 and name HB1))							
ASSI [12901]	3.100	2.400	2.400 peak 12741 weight	0.10000E+01 volume	0.21409E+03 ppm1	7.820 ppm2	2.491
ASSI [12902]							
((segid "BTD" " and readid 42 and name HN))							
((segid "BTD" " and readid 43 and name HB1))							
ASSI [12911]	3.100	2.400	2.400 peak 12741 weight	0.10000E+01 volume	0.21409E+03 ppm1	7.820 ppm2	2.491
ASSI [12912]							
((segid "BTD" " and readid 42 and name HN))							
((segid "BTD" " and readid 43 and name HB1))							
ASSI [12921]	3.100	2.400	2.400 peak 12741 weight	0.10000E+01 volume	0.21409E+03 ppm1	7.820 ppm2	2.491
ASSI [12922]							
((segid "BTD" " and readid 42 and name HN))							
((segid "BTD" " and readid 43 and name HB1))							
ASSI [12931]	3.100	2.400	2.400 peak 12741 weight	0.10000E+01 volume	0.21409E+03 ppm1	7.820 ppm2	2.491
ASSI [12932]							
((segid "BTD" " and readid 42 and name HN))							
((segid "BTD" " and readid 43 and name HB1))							
ASSI [12941]	3.100	2.400	2.400 peak 12741 weight	0.10000E+01 volume	0.21409E+03 ppm1	7.820 ppm2	2.491
ASSI [12942]							
((segid "BTD" " and readid 42 and name HN))							
((segid "BTD" " and readid 43 and name HB1))							
ASSI [12951]	3.100	2.400	2.400 peak 12741 weight	0.10000E+01 volume	0.21409E+03 ppm1	7.820 ppm2	2.491
ASSI [12952]							
((segid "BTD" " and readid 42 and name HN))							
((segid "BTD" " and readid 43 and name HB1))							
ASSI [12961]	3.100	2.400	2.400 peak 12741 weight	0.10000E+01 volume	0.21409E+03 ppm1	7.820 ppm2	2.491
ASSI [12962]							
((segid "BTD" " and readid 42 and name HN))							
((segid "BTD" " and readid 43 and name HB1))							
ASSI [12971]	3.100	2.400	2.400 peak 12741 weight	0.10000E+01 volume	0.21409E+03 ppm1	7.820 ppm2	2.491
ASSI [12972]							
((segid "BTD" " and readid 42 and name HN))							
((segid "BTD" " and readid 43 and name HB1))							
ASSI [12981]	3.100	2.400	2.400 peak 12741 weight	0.10000E+01 volume	0.21409E+03 ppm1	7.820 ppm2	2.491
ASSI [12982]							
((segid "BTD" " and readid 42 and name HN))							

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B **E** **I** **J** **K** **L**

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(( segid "BrD " and resid 59 and name HB2 ))
ASSI (13092) 3.100 2.000 peak 12872 weight 0.10000E+01 volume 0.44554E+02 ppm1 2.484 3.177 ppm2 3.177 ppm2 3.499 4.360 ppm2
(( segid "BrD " and resid 54 and name HB1 ))
(( segid "BrD " and resid 51 and name HB1 ))
(( segid "BrD " and resid 50 and name HB1 ))
ASSI (13112) 3.400 2.900 2.100 peak 13092 weight 0.10000E+01 volume 0.51665E+02 ppm1 1.075 3.288 ppm2 3.288 ppm2 2.344 2.091 ppm2
(( segid "BrD " and resid 73 and name HB2 ))
(( segid "BrD " and resid 72 and name HB2 ))
(( segid "BrD " and resid 71 and name HB2 ))
ASSI (13122) 3.000 2.200 2.200 peak 13112 weight 0.10000E+01 volume 0.10760E+03 ppm1 5.142 2.486 ppm2 2.486 ppm2 5.362 1.402 ppm2
(( segid "BrD " and resid 73 and name HB1 ))
(( segid "BrD " and resid 68 and name HB1 ))
ASSI (13292) 2.100 2.100 peak 13122 weight 0.10000E+01 volume 0.13268E+03 ppm1 5.141 2.593 ppm2 2.593 ppm2 1.987 4.655 ppm2
(( segid "BrD " and resid 46 and name HB1 ))
(( segid "BrD " and resid 38 and name HB1 ))
ASSI (13322) 3.500 3.100 2.000 peak 13322 weight 0.10000E+01 volume 0.45934E+02 ppm1 0.790 3.275 ppm2 3.275 ppm2 4.933 3.667 ppm2
(( segid "BrD " and resid 56 and name HB1 ))
(( segid "BrD " and resid 55 and name HB1 ))
OR (13282) 3.100 2.400 2.400 peak 13282 weight 0.10000E+01 volume 0.86018E+02 ppm1 1.637 4.607 ppm2 4.607 ppm2 2.136 4.459 ppm2
(( segid "BrD " and resid 56 and name HB2 ))
(( segid "BrD " and resid 22 and name HB2 ))
ASSI (13312) 1.600 1.600 peak 13312 weight 0.10000E+01 volume 0.31308E+03 ppm1 2.516 1.648 ppm2 1.648 ppm2 2.218 5.000 ppm2
(( segid "BrD " and resid 25 and name HB1 ))
(( segid "BrD " and resid 25 and name HB2 ))
ASSI (13342) 3.000 2.200 2.200 peak 13342 weight 0.10000E+01 volume 0.10565E+03 ppm1 4.437 2.289 ppm2 2.289 ppm2 4.437 2.289 ppm2
(( segid "BrD " and resid 56 and name HB1 ))
(( segid "BrD " and resid 49 and name HB1 ))
ASSI (13722) 2.900 2.100 2.100 peak 13722 weight 0.10000E+01 volume 0.12726E+03 ppm1 1.252 1.795 ppm2 1.795 ppm2 3.581 4.457 ppm2
(( segid "BrD " and resid 56 and name HB2 ))
(( segid "BrD " and resid 55 and name HB2 ))
ASSI (13582) 5.500 5.500 0.000 peak 13572 weight 0.10000E+01 volume 0.27123E+01 ppm1 1.417 2.634 ppm2 2.634 ppm2 1.318 2.338 ppm2
(( segid "BrD " and resid 49 and name HB1 ))
(( segid "BrD " and resid 49 and name HB2 ))
ASSI (13752) 3.500 3.100 2.000 peak 13752 weight 0.10000E+01 volume 0.44471E+02 ppm1 3.662 5.296 ppm2 5.296 ppm2 2.042 4.606 ppm2
(( segid "BrD " and resid 63 and name HB2 ))
(( segid "BrD " and resid 19 and name HB2 ))
ASSI (13792) 1.600 1.600 peak 13752 weight 0.10000E+01 volume 0.20264E+03 ppm1 1.996 1.498 ppm2 1.498 ppm2 2.181 4.411 ppm2
(( segid "BrD " and resid 63 and name HB1 ))
(( segid "BrD " and resid 64 and name HB1 ))
ASSI (13812) 4.000 4.000 1.500 peak 13772 weight 0.10000E+01 volume 0.18294E+02 ppm1 1.488 4.951 ppm2 4.951 ppm2 1.330 1.254 ppm2
(( segid "BrD " and resid 49 and name HB1 ))
(( segid "BrD " and resid 49 and name HB2 ))
ASSI (13842) 3.800 3.600 1.700 peak 13792 weight 0.10000E+01 volume 0.26015E+02 ppm1 1.009 1.646 ppm2 1.646 ppm2 1.278 1.989 ppm2
(( segid "BrD " and resid 76 and name HB1 ))
(( segid "BrD " and resid 80 and name HB2 ))
ASSI (13862) 4.200 4.200 1.300 peak 13812 weight 0.10000E+01 volume 0.14558E+02 ppm1 2.508 4.656 ppm2 4.656 ppm2 2.351 3.866 ppm2
(( segid "BrD " and resid 56 and name HB1 ))
(( segid "BrD " and resid 34 and name HB2 ))
ASSI (13872) 3.100 2.400 2.400 peak 13812 weight 0.10000E+01 volume 0.92421E+02 ppm1 3.159 2.685 ppm2 2.685 ppm2 2.467 1.057 ppm2
(( segid "BrD " and resid 69 and name HB2 ))
(( segid "BrD " and resid 69 and name HB1 ))
ASSI (13892) 5.500 5.500 0.000 peak 13872 weight 0.10000E+01 volume 0.14355E+01 ppm1 0.860 1.425 ppm2 1.425 ppm2 1.458 1.205 ppm2
(( segid "BrD " and resid 12 and name HB1 ))
(( segid "BrD " and resid 14 and name HB2 ))
OR (13392) 2.200 2.200 peak 13892 weight 0.10000E+01 volume 0.11539E+03 ppm1 1.302 5.298 ppm2 5.298 ppm2 4.222 4.460 ppm2
(( segid "BrD " and resid 12 and name HB2 ))
(( segid "BrD " and resid 14 and name HB1 ))
ASSI (13902) 3.500 3.100 2.000 peak 13902 weight 0.10000E+01 volume 0.60436E+03 ppm1 2.956 5.446 ppm2 5.446 ppm2

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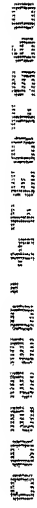

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((segid "BPD" and resid 36 and name HA))	2 900	2 100 peak 27392 weight	0.10000E+01 volume	0.54954E+03 ppm1	2 979 ppm2	5 442
ASSI [27462]						
((segid "BPD" and resid 69 and name H01))	2 400	2 100 peak 27442 weight	0.10000E+01 volume	0.37315E+03 ppm1	1 547 ppm2	1 091
ASSI [27452]						
((segid "BPD" and resid 20 and name H01))	2 400	2 100 peak 27452 weight	0.10000E+01 volume	0.30318E+03 ppm1	1 599 ppm2	1 780
ASSI [27472]						
((segid "BPD" and resid 22 and name H01))	2 400	2 100 peak 27472 weight	0.10000E+01 volume	0.54052E+03 ppm1	1 599 ppm2	3 003
ASSI [27492]						
((segid "BPD" and resid 22 and name H01))	2 400	2 100 peak 27492 weight	0.10000E+01 volume	0.56630E+03 ppm1	1 599 ppm2	4 809
ASSI [27552]						
((segid "BPD" and resid 25 and name H01))	2 400	2 100 peak 27552 weight	0.10000E+01 volume	0.54070E+03 ppm1	1 599 ppm2	7 539
ASSI [27572]						
((segid "BPD" and resid 22 and name H01))	2 400	2 100 peak 27572 weight	0.10000E+01 volume	0.80641E+03 ppm1	1 645 ppm2	4 990
ASSI [27602]						
((segid "BPD" and resid 22 and name H01))	2 400	2 100 peak 27602 weight	0.10000E+01 volume	0.62418E+03 ppm1	1 646 ppm2	7 529
ASSI [27632]						
((segid "BPD" and resid 73 and name H01))	2 400	2 100 peak 27632 weight	0.10000E+01 volume	0.31070E+03 ppm1	1 549 ppm2	5 143
ASSI [27662]						
((segid "BPD" and resid 70 and name H01))	2 400	2 100 peak 27662 weight	0.10000E+01 volume	0.86052E+03 ppm1	1 549 ppm2	4 362
ASSI [27712]						
((segid "BPD" and resid 73 and name H01))	2 400	2 100 peak 27712 weight	0.10000E+01 volume	0.17666E+03 ppm1	1 500 ppm2	2 106
ASSI [27722]						
((segid "BPD" and resid 48 and name HA))	2 400	2 100 peak 27722 weight	0.10000E+01 volume	0.11137E+03 ppm1	4 803 ppm2	1 652
ASSI [27842]						
((segid "BPD" and resid 78 and name H01))	2 400	2 100 peak 27842 weight	0.10000E+01 volume	0.55059E+03 ppm1	2 487 ppm2	4 377
ASSI [27882]						
((segid "BPD" and resid 78 and name H01))	2 400	2 100 peak 27882 weight	0.10000E+01 volume	0.26285E+03 ppm1	3 947 ppm2	3 112
ASSI [27892]						
((segid "BPD" and resid 78 and name H01))	2 400	2 100 peak 27892 weight	0.10000E+01 volume	0.31945E+03 ppm1	1 056 ppm2	1 954
ASSI [27912]						
((segid "BPD" and resid 78 and name H01))	2 400	2 100 peak 27912 weight	0.10000E+01 volume	0.17221E+03 ppm1	1 056 ppm2	4 411
ASSI [27922]						
((segid "BPD" and resid 78 and name H01))	2 400	2 100 peak 27922 weight	0.10000E+01 volume	0.22274E+03 ppm1	1 254 ppm2	4 509
ASSI [27932]						
((segid "BPD" and resid 78 and name H01))	2 400	2 100 peak 27932 weight	0.10000E+01 volume	0.30077E+03 ppm1	1 254 ppm2	7 047
ASSI [27942]						
((segid "BPD" and resid 78 and name H01))	2 400	2 100 peak 27942 weight	0.10000E+01 volume	0.14865E+03 ppm1	1 056 ppm2	7 532
ASSI [27952]						
((segid "BPD" and resid 78 and name H01))	2 400	2 100 peak 27952 weight	0.10000E+01 volume	0.24618E+03 ppm1	0 760 ppm2	7 635
ASSI [27962]						
((segid "BPD" and resid 78 and name H01))	2 400	2 100 peak 27962 weight	0.10000E+01 volume	0.76319E+03 ppm1	0 662 ppm2	7 528
ASSI [27972]						
((segid "BPD" and resid 78 and name H01))	2 400	2 100 peak 27972 weight	0.10000E+01 volume	0.53417E+03 ppm1	0 662 ppm2	7 031
ASSI [27982]						
((segid "BPD" and resid 78 and name H01))	2 400	2 100 peak 27982 weight	0.10000E+01 volume	0.29286E+03 ppm1	2 141 ppm2	7 041
ASSI [27992]						
((segid "BPD" and resid 78 and name H01))	2 400	2 100 peak 27992 weight	0.10000E+01 volume	0.29286E+03 ppm1	2 141 ppm2	7 041
OR [27992]						

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Ambiguous NOE-derived Inter-proton Distance Restraints

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Variable	Mean	SD	Min	Max
Age	38.5	12.5	25	65
Gender	Male	Female		
Marital Status	Married	Single		
Education	High School	College		
Occupation	Manager	Worker		
Income	\$30,000	\$40,000		
Health Status	Good	Fair		
Stress Level	Low	High		
Life Satisfaction	High	Low		
Work-Life Balance	Good	Poor		
Family Support	Strong	Weak		
Community Involvement	Active	Passive		
Religious Beliefs	Religious	Secular		
Political Views	Conservative	Liberal		
Travel Habits	Frequent	Rarely		
Dietary Preferences	Vegetarian	Non-Vegetarian		
Exercise Routine	Regular	Irregular		
Substance Use	None	Occasional		
Artistic Interests	High	Low		
Music Preferences	Classical	Pop		
Gardening Interests	High	Low		
Reading Habits	Frequent	Rarely		
Volunteering	Regular	Occasional		
Charitable Contributions	High	Low		
Philanthropic Interests	High	Low		
Environmental Concerns	High	Low		
Technology Use	High	Low		
Online Activity	Frequent	Rarely		
Mobile Phone Use	High	Low		
Internet Access	High	Low		
Smartphone Ownership	High	Low		
Tablet Ownership	High	Low		
Wearable Device Use	High	Low		
Cloud Storage Use	High	Low		
Online Shopping	Frequent	Rarely		
Digital Privacy Concerns	High	Low		
Online Security Measures	High	Low		
Digital Literacy	High	Low		
Online Learning	Frequent	Rarely		
Digital Communication	Frequent	Rarely		
Online Social Interaction	Frequent	Rarely		
Digital Identity Management	High	Low		
Online Reputation Concerns	High	Low		
Digital Privacy Settings	High	Low		
Online Security Updates	Frequent	Rarely		
Digital Backup Habits	Frequent	Rarely		
Online Data Management	Frequent	Rarely		
Digital File Organization	Frequent	Rarely		
Online Collaboration	Frequent	Rarely		
Digital Project Management	Frequent	Rarely		
Online Teamwork	Frequent	Rarely		
Digital Communication Tools	Frequent	Rarely		
Online Meeting Participation	Frequent	Rarely		
Digital Decision Making	Frequent	Rarely		
Online Problem Solving	Frequent	Rarely		
Digital Learning Outcomes	Frequent	Rarely		
Online Skill Development	Frequent	Rarely		
Digital Career Advancement	Frequent	Rarely		
Online Networking	Frequent	Rarely		
Digital Professional Development	Frequent	Rarely		
Online Industry Connections	Frequent	Rarely		
Digital Business Opportunities	Frequent	Rarely		
Online Entrepreneurship	Frequent	Rarely		
Digital Marketing Strategies	Frequent	Rarely		
Online Brand Management	Frequent	Rarely		
Digital Customer Engagement	Frequent	Rarely		
Online Sales Performance	Frequent	Rarely		
Digital Revenue Growth	Frequent	Rarely		
Online Profitability	Frequent	Rarely		
Digital Business Success	Frequent	Rarely		
Online Market Research	Frequent	Rarely		
Digital Consumer Insights	Frequent	Rarely		
Online Product Development	Frequent	Rarely		
Digital Innovation	Frequent	Rarely		
Online R&D Investment	Frequent	Rarely		
Digital Patent Filings	Frequent	Rarely		
Online Intellectual Property	Frequent	Rarely		
Digital Trademark Protection	Frequent	Rarely		
Online Copyright Management	Frequent	Rarely		
Digital Content Creation	Frequent	Rarely		
Online Media Production	Frequent	Rarely		
Digital Advertising Campaigns	Frequent	Rarely		
Online Marketing Budget	Frequent	Rarely		
Digital Campaign ROI	Frequent	Rarely		
Online Brand Awareness	Frequent	Rarely		
Digital Customer Retention	Frequent	Rarely		
Online Loyalty Programs	Frequent	Rarely		
Digital Feedback Mechanisms	Frequent	Rarely		
Online Customer Service	Frequent	Rarely		
Digital Complaint Resolution	Frequent	Rarely		
Online Reputation Management	Frequent	Rarely		
Digital Crisis Communication	Frequent	Rarely		
Online Public Relations	Frequent	Rarely		
Digital Media Monitoring	Frequent	Rarely		
Online Social Listening	Frequent	Rarely		
Digital Sentiment Analysis	Frequent	Rarely		
Online Trend Analysis	Frequent	Rarely		
Digital Market Segmentation	Frequent	Rarely		
Online Target Audience Identification	Frequent			

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7 781 p1m2	2 374
7 781 p2m2	1 503
7 786 p1m2	2 666
7 783 p2m2	2 211
7 714 p1m2	2 796
7 713 p2m2	2 321
7 713 p1m2	0 763
7 709 p2m2	2 033
7 713 p1m2	1 088
7 692 p1m2	3 512
7 640 p1m2	1 820
7 643 p2m2	1 593

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(( segid "BrD " and resid 38 and name H02 ))
ASSI (( segid "BrD " and resid 74 and name H01 ))
(( segid "BrD " and resid 78 and name H0 ))
OR (( segid "BrD " and resid 82 and name H2 ))
(( segid "BrD " and resid 78 and name H0 ))
ASSI (( 4154 ))
(( segid "BrD " and resid 74 and name H01 ))
(( segid "BrD " and resid 22 and name H01 ))
OR (( segid "BrD " and resid 106 and name H01 ))
(( segid "BrD " and resid 21 and name H01 ))
ASSI (( 4174 ))
(( segid "BrD " and resid 96 and name H01 ))
(( segid "BrD " and resid 100 and name H0 ))
OR (( segid "BrD " and resid 4174 weight 0 10000E+01 volume 0 70341E+03 ppm1
and name H01 ))
OR (( 4174 ))
(( segid "BrD " and resid 34 and name H01 ))
(( segid "BrD " and resid 35 and name H0 ))
OR (( segid "BrD " and resid 15 and name H01 ))
(( segid "BrD " and resid 64 and name H0 ))
OR (( segid "BrD " and resid 15 and name H01 ))
(( segid "BrD " and resid 11 and name H0 ))
OR (( 4174 ))
(( segid "BrD " and resid 34 and name H01 ))
ASSI (( 4224 ))
(( segid "BrD " and resid 86 and name H01 ))
(( segid "BrD " and resid 50 and name H01 ))
OR (( segid "BrD " and resid 4224 weight 0 10000E+01 volume 0 12637E+03 ppm1
and name H01 ))
OR (( 4224 ))
(( segid "BrD " and resid 95 and name H01 ))
ASSI (( segid "BrD " and resid 33 and name H01 ))
(( segid "BrD " and resid 96 and name H01 ))
(( segid "BrD " and resid 99 and name H01 ))
OR (( segid "BrD " and resid 4234 weight 0 10000E+01 volume 0 94963E+02 ppm1
and name H01 ))
OR (( 4234 ))
(( segid "BrD " and resid 106 and name H01 ))
(( segid "BrD " and resid 16 and name H01 ))
OR (( 4234 ))
(( segid "BrD " and resid 106 and name H01 ))
(( segid "BrD " and resid 109 and name H02 ))
OR (( 4234 ))
(( segid "BrD " and resid 106 and name H01 ))
(( segid "BrD " and resid 115 and name H01 ))
OR (( segid "BrD " and resid 106 and name H01 ))
(( segid "BrD " and resid 115 and name H0 ))
ASSI (( 4244 ))
(( segid "BrD " and resid 106 and name H01 ))
(( segid "BrD " and resid 4244 weight 0 10000E+01 volume 0 14612E+03 ppm1
and name H01 ))
OR (( segid "BrD " and resid 96 and name H01 ))
(( segid "BrD " and resid 96 and name H02 ))
ASSI (( 4284 ))
(( segid "BrD " and resid 74 and name H01 ))
(( segid "BrD " and resid 74 and name H02 ))
OR (( segid "BrD " and resid 4284 weight 0 10000E+01 volume 0 18031E+03 ppm1
and name H01 ))
OR (( 4284 ))
(( segid "BrD " and resid 106 and name H01 ))
(( segid "BrD " and resid 109 and name H02 ))
ASSI (( 4344 ))
(( segid "BrD " and resid 34 and name H0 ))
(( segid "BrD " and resid 38 and name H02 ))
OR (( segid "BrD " and resid 4344 weight 0 10000E+01 volume 0 12962E+03 ppm1
and name H01 ))
OR (( 4344 ))
(( segid "BrD " and resid 68 and name H01 ))
ASSI (( segid "BrD " and resid 54 and name H0 ))
(( segid "BrD " and resid 106 and name H01 ))
(( segid "BrD " and resid 78 and name H02 ))
OR (( segid "BrD " and resid 4354 weight 0 10000E+01 volume 0 19182E+03 ppm1
and name H01 ))
OR (( 4354 ))
(( segid "BrD " and resid 74 and name H01 ))
(( segid "BrD " and resid 18 and name H01 ))
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Table 4

Hydrogen Bonding Restraints

!Helix Z						
assign (residue 19 and name HN)	(residue 15 and name O)	1.80	0.0	0.40		
assign (residue 19 and name N)	(residue 15 and name O)	2.80	0.30	0.40		
assign (residue 22 and name HN)	(residue 18 and name O)	1.80	0.0	0.40		
assign (residue 22 and name N)	(residue 18 and name O)	2.80	0.30	0.40		
assign (residue 23 and name HN)	(residue 19 and name O)	1.80	0.0	0.40		
assign (residue 23 and name N)	(residue 19 and name O)	2.80	0.30	0.40		
assign (residue 24 and name HN)	(residue 20 and name O)	1.80	0.0	0.40		
assign (residue 24 and name N)	(residue 20 and name O)	2.80	0.30	0.40		
assign (residue 25 and name HN)	(residue 21 and name O)	1.80	0.0	0.40		
assign (residue 25 and name N)	(residue 21 and name O)	2.80	0.30	0.40		
!Helix B						
assign (residue 75 and name HN)	(residue 71 and name O)	1.80	0.0	0.40		
assign (residue 75 and name N)	(residue 71 and name O)	2.80	0.30	0.40		
!assign (residue 77 and name HN)	(residue 73 and name O)	1.80	0.0	0.40		
!assign (residue 77 and name N)	(residue 73 and name O)	2.80	0.30	0.40		
assign (residue 78 and name HN)	(residue 74 and name O)	1.80	0.0	0.40		
assign (residue 78 and name N)	(residue 74 and name O)	2.80	0.30	0.40		
assign (residue 79 and name HN)	(residue 75 and name O)	1.80	0.0	0.40		
assign (residue 79 and name N)	(residue 75 and name O)	2.80	0.30	0.40		
!assign (residue 80 and name HN)	(residue 76 and name O)	1.80	0.0	0.40		
!assign (residue 80 and name N)	(residue 76 and name O)	2.80	0.30	0.40		
assign (residue 81 and name HN)	(residue 77 and name O)	1.80	0.0	0.40		
assign (residue 81 and name N)	(residue 77 and name O)	2.80	0.30	0.40		
assign (residue 82 and name HN)	(residue 78 and name O)	1.80	0.0	0.40		
assign (residue 82 and name N)	(residue 78 and name O)	2.80	0.30	0.40		
!Helix C						
assign (residue 102 and name HN)	(residue 98 and name O)	1.80	0.0	0.40		
assign (residue 102 and name N)	(residue 98 and name O)	2.80	0.30	0.40		
assign (residue 103 and name HN)	(residue 99 and name O)	1.80	0.0	0.40		
assign (residue 103 and name N)	(residue 99 and name O)	2.80	0.30	0.40		
assign (residue 104 and name HN)	(residue 100 and name O)	1.80	0.0	0.40		
assign (residue 104 and name N)	(residue 100 and name O)	2.80	0.30	0.40		
assign (residue 105 and name HN)	(residue 101 and name O)	1.80	0.0	0.40		
assign (residue 105 and name N)	(residue 101 and name O)	2.80	0.30	0.40		

Table 5

Atomic Structure Coordinates of the Free Form of the p/CAF Bromodomain

[illegible]

ATOM	67	N	LVS	6	23.756	3.805	-5.600	1.00	0.00	161	HGI	PRO	11	15.582	-6.715	-3.188	1.00	0.00
ATOM	68	NN	LVS	6	23.532	3.650	-5.520	1.00	0.00	162	HN	PRO	11	14.224	-5.561	-3.666	1.00	0.00
ATOM	69	CA	LVS	6	21.987	2.660	-6.318	1.00	0.00	163	CD	PRO	11	14.224	-5.561	-3.666	1.00	0.00
ATOM	70	HA	LVS	6	21.642	2.942	-7.308	1.00	0.00	164	CD	PRO	11	16.155	-4.133	-3.555	1.00	0.00
ATOM	71	CH	LVS	6	22.669	1.413	-6.409	1.00	0.00	165	HD2	PRO	11	16.911	-5.056	-2.237	1.00	0.00
ATOM	72	HB	LVS	6	22.655	0.563	-6.232	1.00	0.00	166	C	PRO	11	14.732	-4.881	0.572	1.00	0.00
ATOM	73	HB2	LVS	6	23.655	0.563	-6.232	1.00	0.00	167	O	PRO	11	13.991	-5.446	1.375	1.00	0.00
ATOM	74	CG	LVS	6	23.510	2.338	-7.773	1.00	0.00	168	HN	ASR	12	14.477	-5.394	0.912	1.00	0.00
ATOM	75	HGI	LVS	6	24.045	3.238	-8.041	1.00	0.00	169	HN	ASR	12	14.477	-5.394	0.912	1.00	0.00
ATOM	76	HG2	LVS	6	24.201	0.409	-7.721	1.00	0.00	170	CA	ASR	12	16.430	-4.808	2.576	1.00	0.00
ATOM	77	HG2	LVS	6	24.201	0.409	-7.721	1.00	0.00	171	HA	ASR	12	16.402	-5.551	2.554	1.00	0.00
ATOM	78	HD1	LVS	6	22.469	0.947	-8.642	1.00	0.00	172	CB	ASR	12	17.874	-4.008	2.352	1.00	0.00
ATOM	79	HD2	LVS	6	22.970	0.604	-8.788	1.00	0.00	173	CB	ASR	12	15.146	-3.873	3.369	1.00	0.00
ATOM	80	CE	LVS	6	21.669	-0.304	-8.814	1.00	0.00	174	HB2	ASR	12	15.146	-3.873	3.369	1.00	0.00
ATOM	81	HE1	LVS	6	21.107	-0.503	-8.327	1.00	0.00	175	CG	ASR	12	18.856	-4.975	1.929	1.00	0.00
ATOM	82	HE2	LVS	6	23.346	-1.489	-8.317	1.00	0.00	176	OD1	ASR	12	18.856	-4.975	1.929	1.00	0.00
ATOM	84	H23	LVS	6	21.939	-2.365	-8.435	1.00	0.00	177	OD2	ASR	12	19.615	-6.157	2.125	1.00	0.00
ATOM	85	H23	LVS	6	22.958	1.476	-7.352	1.00	0.00	178	C	ASR	12	13.012	-1.546	4.191	1.00	0.00
ATOM	86	H23	LVS	6	22.958	1.476	-7.352	1.00	0.00	179	C	ASR	12	13.012	-1.546	4.191	1.00	0.00
ATOM	87	C	LVS	6	20.776	2.397	-9.436	1.00	0.00	180	CA	GLN	13	15.115	-1.923	5.197	1.00	0.00
ATOM	88	N	GLU	7	19.637	3.601	-6.552	1.00	0.00	181	HA	GLN	13	15.115	-1.923	5.197	1.00	0.00
ATOM	89	NN	GLU	7	19.637	3.601	-6.552	1.00	0.00	182	HA	GLN	13	15.115	-1.923	5.197	1.00	0.00
ATOM	90	HN	GLU	7	18.431	2.825	-5.005	1.00	0.00	183	CA	GLN	13	15.115	-1.923	5.197	1.00	0.00
ATOM	91	CA	GLU	7	18.431	2.825	-5.005	1.00	0.00	184	CA	GLN	13	15.115	-1.923	5.197	1.00	0.00
ATOM	92	HA	GLU	7	18.200	4.011	-8.064	1.00	0.00	185	HA	GLN	13	15.115	-1.923	5.197	1.00	0.00
ATOM	93	CB	GLU	7	18.120	1.352	-7.702	1.00	0.00	186	HB2	GLN	13	15.288	-0.025	6.246	1.00	0.00
ATOM	94	HB	PRO	8	16.120	1.352	-7.702	1.00	0.00	187	CG	GLN	13	15.336	0.669	5.626	1.00	0.00
ATOM	95	HB2	PRO	8	16.760	0.416	-8.757	1.00	0.00	188	HGI	GLN	13	15.288	-0.025	6.246	1.00	0.00
ATOM	96	CG	GLU	7	18.976	3.904	-2.763	1.00	0.00	189	HG2	GLN	13	14.403	1.208	5.347	1.00	0.00
ATOM	97	HGI	GLU	7	19.746	3.156	-2.876	1.00	0.00	190	HD1	GLN	13	16.450	1.662	5.687	1.00	0.00
ATOM	98	HG2	GLU	7	19.430	4.860	-2.548	1.00	0.00	191	OD1	GLN	13	16.930	1.495	4.725	1.00	0.00
ATOM	99	HD2	GLU	7	18.095	3.515	-1.589	1.00	0.00	192	NE2	GLN	13	17.651	2.428	1.125	1.00	0.00
ATOM	100	OD1	GLU	7	18.343	2.243	-3.312	1.00	0.00	193	HE21	GLN	13	16.543	1.085	7.587	1.00	0.00
ATOM	101	OD2	GLU	7	17.215	2.662	-6.928	1.00	0.00	194	CE22	GLN	13	16.543	1.085	7.587	1.00	0.00
ATOM	102	C	GLU	7	16.278	3.461	-5.886	1.00	0.00	195	C	GLN	13	13.538	-1.566	3.907	1.00	0.00
ATOM	103	O	PRO	8	17.218	1.617	-6.772	1.00	0.00	196	N	LEU	14	13.058	-1.499	4.666	1.00	0.00
ATOM	104	N	PRO	8	16.120	1.352	-7.702	1.00	0.00	197	N	LEU	14	13.058	-1.499	4.666	1.00	0.00
ATOM	105	HA	PRO	8	16.760	0.416	-8.757	1.00	0.00	198	HN	LEU	14	14.025	-1.723	1.677	1.00	0.00
ATOM	106	CA	PRO	8	16.760	0.416	-8.757	1.00	0.00	199	HN	LEU	14	14.025	-1.723	1.677	1.00	0.00
ATOM	107	HB	PRO	8	16.760	0.416	-8.757	1.00	0.00	200	CA	LEU	14	11.914	-1.713	1.999	1.00	0.00
ATOM	108	HBI	PRO	8	17.200	1.002	-9.523	1.00	0.00	201	CA	LEU	14	11.445	-0.764	2.212	1.00	0.00
ATOM	109	HBI	PRO	8	16.011	-0.245	-9.130	1.00	0.00	202	HB2	LEU	14	11.939	-1.932	0.481	1.00	0.00
ATOM	110	CG	PRO	8	17.796	-0.327	-7.958	1.00	0.00	203	HB2	LEU	14	11.939	-1.932	0.481	1.00	0.00
ATOM	111	CG	PRO	8	16.507	-1.205	-7.508	1.00	0.00	204	CG	LEU	14	12.702	-2.642	0.912	1.00	0.00
ATOM	112	HG2	PRO	8	18.429	0.613	-6.889	1.00	0.00	205	HG	LEU	14	10.635	-2.407	-0.145	1.00	0.00
ATOM	113	CD	PRO	8	18.294	0.613	-6.889	1.00	0.00	206	HG	LEU	14	9.801	-1.900	0.313	1.00	0.00
ATOM	114	HD1	PRO	8	18.429	0.613	-6.889	1.00	0.00	207	CD1	LEU	14	11.502	-2.066	-1.628	1.00	0.00
ATOM	115	HD2	PRO	8	19.220	1.076	-7.127	1.00	0.00	208	CD1	LEU	14	11.502	-2.066	-1.628	1.00	0.00
ATOM	116	C	PRO	8	14.938	0.669	-7.031	1.00	0.00	209	HD21	LEU	14	10.396	-2.403	-0.098	1.00	0.00
ATOM	117	C	PRO	8	15.236	-0.364	-6.057	1.00	0.00	210	HD21	LEU	14	9.749	-2.556	-2.091	1.00	0.00
ATOM	118	N	ARG	9	15.236	-0.364	-6.057	1.00	0.00	211	HD21	LEU	14	10.444	-3.902	0.064	1.00	0.00
ATOM	119	HN	ARG	9	16.176	0.357	-5.833	1.00	0.00	212	HD21	LEU	14	11.402	-4.354	0.275	1.00	0.00
ATOM	120	CA	ARG	9	14.199	-0.917	-5.328	1.00	0.00	213	HD21	LEU	14	10.026	-4.344	-0.828	1.00	0.00
ATOM	121	CA	ARG	9	13.522	-0.169	-4.906	1.00	0.00	214	C	LEU	14	11.121	-5.211	0.897	1.00	0.00
ATOM	122	HA	ARG	9	13.421	-1.830	-6.279	1.00	0.00	215	O	LEU	14	10.019	-2.595	3.188	1.00	0.00
ATOM	123	HBI	ARG	9	13.421	-1.830	-6.279	1.00	0.00	216	HN	TVR	15	11.697	-4.018	2.715	1.00	0.00
ATOM	124	HB2	ARG	9	12.978	-1.222	-6.898	1.00	0.00	217	HN	TVR	15	12.579	-4.131	3.203	1.00	0.00
ATOM	125	CG	ARG	9	14.313	-2.661	-7.188	1.00	0.00	218	HN	TVR	15	11.061	-5.167	3.350	1.00	0.00
ATOM	126	HG1	ARG	9	14.295	-2.236	-8.181	1.00	0.00	219	HA	TVR	15	11.061	-5.167	3.350	1.00	0.00
ATOM	127	HG2	ARG	9	15.322	-2.640	-6.803	1.00	0.00	220	CA	TVR	15	11.964	-6.394	3.318	1.00	0.00
ATOM	128	HB2	ARG	9	13.833	-4.506	-7.262	1.00	0.00	221	HBI	TVR	15	12.163	-6.569	2.723	1.00	0.00
ATOM	129	HD1	ARG	9	13.833	-4.506	-7.262	1.00	0.00	222	HBI	TVR	15	12.163	-6.569	2.723	1.00	0.00
ATOM	130	NE	ARG	9	12.844	-4.125	-7.671	1.00	0.00	223	CG	TVR	15	11.374	-7.659	3.798	1.00	0.00
ATOM	131	NE	ARG	9	14.714	-8.926	-8.102	1.00	0.00	224	CG	TVR	15	11.374	-7.659	3.798	1.00	0.00
ATOM	132	HE	ARG	9	15.302	-4.464	-8.735	1.00	0.00	225	HD1	TVR	15	13.058	-8.408	7.734	1.00	0.00
ATOM	133	HE	ARG	9	14.745	-6.255	-8.053	1.00	0.00	226	HD2	TVR	15	13.058	-8.408	7.734	1.00	0.00
ATOM	134	HN	ARG	9	13.342	-6.401	-7.408	1.00	0.00	227	HD2	TVR	15	10.321	-6.111	3.402	1.00	0.00
ATOM	135	HB11	ARG	9	13.985	-7.907	-7.172	1.00	0.00	228	CE1	TVR	15	9.564	-7.543	2.671	1.00	0.00
ATOM	136	HB12	ARG	9	13.985	-7.907	-7.172	1.00	0.00	229	CE1	TVR	15	11.542	-9.565	2.568	1.00	0.00
ATOM	137	HB2	ARG	9	16.157	-6.444	-9.489	1.00	0.00	230	HN	TVR	15	12.163	-6.569	2.723	1.00	0.00
ATOM	138	HB21	ARG	9	15.585	-7.931	-8.810	1.00	0.00	231	HN	TVR	15	9.761	-11.145	3.388	1.00	0.00
ATOM	139	HB22	ARG	9	15.585	-7.931	-8.810	1.00	0.00	232	HN	TVR	15	10.392	-11.963	3.295	1.00	0.00
ATOM	140	C	ARG	9	14.421	-2.897	-7.991	1.00	0.00	233	HN	TVR	15	10.392	-11.963	3.295	1.00	0.00
ATOM	141	O	ARG	9	14.421	-2.897	-7.991	1.00	0.00	234	HN	TVR	15	10.392	-11.963	3.295	1.00	0.00
ATOM	142	N	ASP	10	15.732	-1.144	-3.458	1.00	0.00	235	O	LEU	14	11.694	-4.181	5.471	1.00	0.00
ATOM	143	HN	ASP	10	15.986	-0.223	-3.673	1.00	0.00	236	N	SER	16	11.694	-4.181	5.471	1.00	0.00
ATOM	144	HA	ASP	10	16.393	-1.884	-2.345	1.00										

ATOM	256	H0I THR	17	10.088	1.232	0.832	4.703	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
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ATOM	537	CD1	PHE	34	-6.937	0.784	3.361	1.00	0.00	ATOM	631	C	LVS	39	-14.339	-9.563	-6.469	1.00	0.00	ATOM	725	CD1	TYR	46	-10.623	-1.931	-7.799	1.00	0.00
ATOM	538	HD1	PHE	34	-7.634	0.525	4.946	1.00	0.00	ATOM	632	Q	LVS	39	-13.886	-10.337	-7.278	1.00	0.00	ATOM	726	HD1	TYR	46	-9.964	-2.690	-8.196	1.00	0.00
ATOM	539	CD2	PHE	34	-5.300	0.255	4.946	1.00	0.00	ATOM	633	HN	ARG	40	-15.810	-8.550	-6.074	1.00	0.00	ATOM	727	CD2	TYR	46	-12.432	-0.408	-8.095	1.00	0.00
ATOM	540	HD2	PHE	34	-4.611	-0.459	5.373	1.00	0.00	ATOM	634	HN	ARG	40	-15.810	-8.550	-6.074	1.00	0.00	ATOM	728	CD2	TYR	46	-13.194	0.029	-8.754	1.00	0.00
ATOM	541	CD1	PHE	34	-7.029	0.277	3.868	1.00	0.00	ATOM	635	HA	ARG	40	-16.078	-8.826	-6.074	1.00	0.00	ATOM	729	CD1	TYR	46	-9.725	-1.960	-5.859	1.00	0.00
ATOM	542	HE1	PHE	34	-7.761	2.789	3.443	1.00	0.00	ATOM	636	HA	ARG	40	-15.347	-8.504	-8.800	1.00	0.00	ATOM	730	HE1	TYR	46	-12.303	0.007	-6.783	1.00	0.00
ATOM	543	HE2	PHE	34	-8.726	1.836	2.459	1.00	0.00	ATOM	637	CB	ARG	40	-16.534	-10.246	-8.417	1.00	0.00	ATOM	731	CE2	TYR	46	-12.964	0.766	-6.389	1.00	0.00
ATOM	544	HE2	PHE	34	-6.252	2.450	4.917	1.00	0.00	ATOM	638	HE1	ARG	40	-15.676	-10.822	-8.729	1.00	0.00	ATOM	732	CE2	TYR	46	-11.330	-0.953	-5.983	1.00	0.00
ATOM	545	CE2	PHE	34	-6.304	3.483	5.314	1.00	0.00	ATOM	639	CB	ARG	40	-17.196	-10.968	-7.254	1.00	0.00	ATOM	733	CE2	TYR	46	-10.897	-0.173	-4.576	1.00	0.00
ATOM	546	C	PHE	34	-7.400	-3.344	3.053	1.00	0.00	ATOM	640	CG	ARG	40	-18.190	-10.565	-7.115	1.00	0.00	ATOM	734	HN	TYR	46	-10.427	-0.671	-12.236	1.00	0.00
ATOM	547	C	PHE	34	-7.293	-4.349	2.065	1.00	0.00	ATOM	641	HD1	ARG	40	-16.612	-10.809	-6.363	1.00	0.00	ATOM	735	HN	TYR	46	-11.940	-0.764	-13.371	1.00	0.00
ATOM	548	HN	MET	35	-7.537	-5.534	5.285	1.00	0.00	ATOM	642	HD2	ARG	40	-17.105	-12.462	-7.516	1.00	0.00	ATOM	736	C	TYR	46	-10.120	-0.506	-13.072	1.00	0.00
ATOM	549	HN	MET	35	-7.537	-5.534	5.285	1.00	0.00	ATOM	643	CD	ARG	40	-16.418	-12.788	-8.038	1.00	0.00	ATOM	737	N	TYR	46	-9.772	-0.440	-11.159	1.00	0.00
ATOM	550	HN	MET	35	-7.537	-5.534	5.285	1.00	0.00	ATOM	644	HD1	ARG	40	-16.418	-12.788	-8.038	1.00	0.00	ATOM	738	N	TYR	46	-9.772	-0.440	-11.159	1.00	0.00
ATOM	551	HN	MET	35	-7.537	-5.534	5.285	1.00	0.00	ATOM	645	HN	ARG	40	-17.433	-13.235	-6.273	1.00	0.00	ATOM	739	HN	TYR	46	-9.189	-0.422	-13.185	1.00	0.00
ATOM	552	HA	MET	35	-6.624	-5.948	4.283	1.00	0.00	ATOM	646	HN	ARG	40	-17.433	-13.235	-6.273	1.00	0.00	ATOM	740	HA	TYR	46	-9.433	-1.565	-14.181	1.00	0.00
ATOM	553	HA	MET	35	-6.624	-5.948	4.283	1.00	0.00	ATOM	647	HE	ARG	40	-17.683	-13.735	-5.466	1.00	0.00	ATOM	741	CB	TYR	46	-9.433	-1.565	-14.181	1.00	0.00
ATOM	554	HE1	MET	35	-8.472	-4.988	6.110	1.00	0.00	ATOM	648	CD	ARG	40	-17.235	-14.537	-6.197	1.00	0.00	ATOM	742	CB	TYR	46	-10.224	-1.285	-14.860	1.00	0.00
ATOM	555	HE1	MET	35	-8.472	-4.988	6.110	1.00	0.00	ATOM	649	HN1	ARG	40	-16.898	-15.225	-7.279	1.00	0.00	ATOM	743	HN1	TYR	46	-8.529	-1.745	-14.743	1.00	0.00
ATOM	556	HE2	MET	35	-8.415	-5.929	6.110	1.00	0.00	ATOM	650	HN1	ARG	40	-16.794	-14.758	-8.157	1.00	0.00	ATOM	744	HE2	TYR	46	-9.833	-2.862	-13.514	1.00	0.00
ATOM	557	HE2	MET	35	-8.415	-5.929	6.110	1.00	0.00	ATOM	651	HN2	ARG	40	-16.794	-14.758	-8.157	1.00	0.00	ATOM	745	CD	TYR	46	-9.833	-2.862	-13.514	1.00	0.00
ATOM	558	HD1	MET	35	-6.714	-5.567	7.730	1.00	0.00	ATOM	652	HN2	ARG	40	-17.624	-14.644	-4.216	1.00	0.00	ATOM	746	CD1	TYR	46	-10.756	-3.711	-14.105	1.00	0.00
ATOM	559	HD1	MET	35	-6.714	-5.567	7.730	1.00	0.00	ATOM	653	HN2	ARG	40	-17.624	-14.644	-4.216	1.00	0.00	ATOM	747	CD1	TYR	46	-10.756	-3.711	-14.105	1.00	0.00
ATOM	560	HD2	MET	35	-5.766	-5.567	6.278	1.00	0.00	ATOM	654	HN2	ARG	40	-17.220	-16.147	-4.976	1.00	0.00	ATOM	748	CD2	TYR	46	-9.280	-0.538	-13.257	1.00	0.00
ATOM	561	HD2	MET	35	-5.766	-5.567	6.278	1.00	0.00	ATOM	655	C	ARG	40	-17.268	-7.874	-8.116	1.00	0.00	ATOM	749	CD2	TYR	46	-8.572	-2.579	-11.836	1.00	0.00
ATOM	562	HA	MET	35	-6.236	-7.591	7.437	1.00	0.00	ATOM	656	C	ARG	40	-17.442	-7.322	-9.074	1.00	0.00	ATOM	750	CE1	TYR	46	-11.124	-4.899	-13.496	1.00	0.00
ATOM	563	HA	MET	35	-6.236	-7.591	7.437	1.00	0.00	ATOM	657	HN	THR	41	-17.442	-7.322	-9.074	1.00	0.00	ATOM	751	HE1	TYR	46	-11.843	-5.550	-13.971	1.00	0.00
ATOM	564	C	MET	35	-8.656	-6.194	3.674	1.00	0.00	ATOM	658	HN	THR	41	-18.081	-7.910	-7.065	1.00	0.00	ATOM	752	CE2	TYR	46	-9.653	-4.411	-11.674	1.00	0.00
ATOM	565	C	MET	35	-8.656	-6.194	3.674	1.00	0.00	ATOM	659	HN	THR	41	-18.081	-7.910	-7.065	1.00	0.00	ATOM	753	CE2	TYR	46	-9.653	-4.411	-11.674	1.00	0.00
ATOM	566	HA	GLU	36	-9.253	-7.208	2.671	1.00	0.00	ATOM	660	HA	THR	41	-19.528	-6.751	-7.973	1.00	0.00	ATOM	754	CD	TYR	46	-10.570	-4.742	-13.222	1.00	0.00
ATOM	567	HA	GLU	36	-9.253	-7.208	2.671	1.00	0.00	ATOM	661	HA	THR	41	-19.528	-6.751	-7.973	1.00	0.00	ATOM	755	CD	TYR	46	-10.570	-4.742	-13.222	1.00	0.00
ATOM	568	HA	GLU	36	-8.598	-6.569	1.409	1.00	0.00	ATOM	662	HB	THR	41	-20.418	-7.806	-6.135	1.00	0.00	ATOM	756	HN	TYR	46	-10.934	-6.421	-11.671	1.00	0.00
ATOM	569	HA	GLU	36	-8.598	-6.569	1.409	1.00	0.00	ATOM	663	HB	THR	41	-20.418	-7.806	-6.135	1.00	0.00	ATOM	757	HN	TYR	46	-10.934	-6.421	-11.671	1.00	0.00
ATOM	570	CB	GLU	36	-10.371	-8.248	2.562	1.00	0.00	ATOM	664	HB	THR	41	-21.586	-7.003	-6.313	1.00	0.00	ATOM	758	Q	TYR	46	-9.318	0.217	-13.916	1.00	0.00
ATOM	571	HB1	GLU	36	-11.351	-7.504	2.496	1.00	0.00	ATOM	665	CG2	THR	41	-21.586	-7.003	-6.313	1.00	0.00	ATOM	759	Q	TYR	46	-9.318	0.217	-13.916	1.00	0.00
ATOM	572	HB2	GLU	36	-10.322	-8.406	3.601	1.00	0.00	ATOM	666	CG2	THR	41	-21.586	-7.003	-6.313	1.00	0.00	ATOM	760	HN	GLU	48	-10.227	0.558	-14.451	1.00	0.00
ATOM	573	HB2	GLU	36	-10.322	-8.406	3.601	1.00	0.00	ATOM	667	HB2	THR	41	-21.586	-7.003	-6.313	1.00	0.00	ATOM	761	HN	GLU	48	-10.227	0.558	-14.451	1.00	0.00
ATOM	574	HB3	GLU	36	-11.473	-9.338	1.105	1.00	0.00	ATOM	668	HB3	THR	41	-21.586	-7.003	-6.313	1.00	0.00	ATOM	762	HA	GLU	48	-10.754	-2.425	-15.175	1.00	0.00
ATOM	575	HB3	GLU	36	-11.473	-9.338	1.105	1.00	0.00	ATOM	669	HB3	THR	41	-21.586	-7.003	-6.313	1.00	0.00	ATOM	763	HA	GLU	48	-10.754	-2.425	-15.175	1.00	0.00
ATOM	576	CD	GLU	36	-11.806	-10.289	2.976	1.00	0.00	ATOM	670	HN	GLU	42	-18.940	-5.787	-6.156	1.00	0.00	ATOM	764	HB1	GLU	48	-12.209	-2.478	-15.648	1.00	0.00
ATOM	577	CD	GLU	36	-11.806	-10.289	2.976	1.00	0.00	ATOM	671	HN	GLU	42	-18.940	-5.787	-6.156	1.00	0.00	ATOM	765	CD	GLU	48	-12.209	-2.478	-15.648	1.00	0.00
ATOM	578	CE2	GLU	36	-12.794	-9.685	3.440	1.00	0.00	ATOM	672	HN	GLU	42	-18.940	-5.787	-6.156	1.00	0.00	ATOM	766	CD	GLU	48	-12.209	-2.478	-15.648	1.00	0.00
ATOM	579	CE2	GLU	36	-12.794	-9.685	3.440	1.00	0.00	ATOM	673	HN	GLU	42	-18.940	-5.787	-6.156	1.00	0.00	ATOM	767	HN1	GLU	48	-12.135	1.337	-17.444	1.00	0.00
ATOM	580	C	GLU	36	-10.543	-6.792	0.696	1.00	0.00	ATOM	674	HA	GLU	42	-17.570	-4.797	-4.408	1.00	0.00	ATOM	768	HN2	GLU	48	-12.304	0.376	-15.976	1.00	0.00
ATOM	581	N	PRO	37	-8.913	-6.929	0.848	1.00	0.00	ATOM	675	HA	GLU	42	-17.570	-4.797	-4.408	1.00	0.00	ATOM	769	HN2	GLU	48	-12.304	0.376	-15.976	1.00	0.00
ATOM	582	N	PRO	37	-8.913	-6.929	0.848	1.00	0.00	ATOM	676	HB	GLU	42	-18.437	-4.480	-3.847	1.00	0.00	ATOM	770	CE1	GLU	48	-14.120	1.204	-16.702	1.00	0.00
ATOM	583	HA	PRO	37	-9.135	-5.029	-1.386	1.00	0.00	ATOM	677	HB	GLU	42	-18.437	-4.480	-3.847	1.00	0.00	ATOM	771	CE1	GLU	48	-14.120	1.204	-16.702	1.00	0.00
ATOM	584	HA	PRO	37	-9.135	-5.029	-1.386	1.00	0.00	ATOM	678	CG	GLU	42	-16.561	-4.556	-2.976	1.00	0.00	ATOM	772	C	GLU	48	-14.544	0.939	-15.994	1.00	0.00
ATOM	585	N	VAL	38	-7.650	-5.515	-3.031	1.00	0.00	ATOM	679	HB1	GLU	42	-17.313	-5.054</													

ATOM	819	CD	ARG	51	-2.433	-4.849	-11.240	1.00	0.00	ATOM	913	CG	LVS	57	-6.542	-10.935	9.520	1.00	0.00	ATOM	1007	C	ARG	62	4.700	-11.542	-0.664	1.00	0.00
ATOM	820	HD	ARG	51	-2.996	5.010	-10.332	1.00	0.00	ATOM	914	CG	LVS	57	-6.542	-10.935	9.520	1.00	0.00	ATOM	1008	C	ARG	62	5.731	-12.742	-0.664	1.00	0.00
ATOM	821	HD2	ARG	51	-1.566	5.493	-11.244	1.00	0.00	ATOM	915	HD2	LVS	57	-7.622	-10.950	2.517	1.00	0.00	ATOM	1009	N	LEU	63	4.700	-10.366	-0.052	1.00	0.00
ATOM	822	HE	ARG	51	-3.275	5.184	-12.385	1.00	0.00	ATOM	916	CD	LVS	57	-6.049	-11.720	3.735	1.00	0.00	ATOM	1010	HN	LEU	63	3.882	-9.149	0.768	1.00	0.00
ATOM	823	HE	ARG	51	-3.275	5.184	-12.385	1.00	0.00	ATOM	917	HD1	LVS	57	-5.947	-11.047	4.572	1.00	0.00	ATOM	1011	CA	LEU	63	5.792	-9.853	0.768	1.00	0.00
ATOM	824	CH	ARG	51	-2.832	5.236	-12.212	1.00	0.00	ATOM	918	HD2	LVS	57	-5.947	-11.047	4.572	1.00	0.00	ATOM	1012	HA	LEU	63	6.584	-9.663	0.117	1.00	0.00
ATOM	825	CH	ARG	51	-1.562	4.953	-13.904	1.00	0.00	ATOM	919	HD2	LVS	57	-5.947	-11.047	4.572	1.00	0.00	ATOM	1013	HA	LEU	63	6.584	-9.663	0.117	1.00	0.00
ATOM	826	HE1	ARG	51	-1.231	4.984	-14.846	1.00	0.00	ATOM	920	HE1	LVS	57	-7.967	-12.640	3.635	1.00	0.00	ATOM	1014	HE1	LEU	63	5.208	-7.805	0.882	1.00	0.00
ATOM	827	HE1	ARG	51	-0.936	4.716	-13.161	1.00	0.00	ATOM	921	HE2	LVS	57	-6.621	-13.771	3.759	1.00	0.00	ATOM	1015	HE2	LEU	63	4.460	-8.716	1.982	1.00	0.00
ATOM	828	HE1	ARG	51	-3.459	5.539	-14.426	1.00	0.00	ATOM	922	HE2	LVS	57	-7.223	-12.935	5.585	1.00	0.00	ATOM	1016	CG	LEU	63	6.413	-7.984	2.436	1.00	0.00
ATOM	829	HE2	ARG	51	-3.459	5.539	-14.426	1.00	0.00	ATOM	923	HE2	LVS	57	-6.463	-12.609	6.084	1.00	0.00	ATOM	1017	CG	LEU	63	7.141	-8.747	2.663	1.00	0.00
ATOM	830	HE2	ARG	51	-4.617	5.746	-14.430	1.00	0.00	ATOM	924	HE2	LVS	57	-6.463	-12.609	6.084	1.00	0.00	ATOM	1018	CG	LEU	63	7.141	-8.747	2.663	1.00	0.00
ATOM	831	C	ARG	51	-3.684	6.034	-13.056	1.00	0.00	ATOM	925	C	LVS	57	-8.355	-10.144	1.617	1.00	0.00	ATOM	1019	HD1	LEU	63	6.487	-5.604	1.025	1.00	0.00
ATOM	832	O	ARG	51	-4.094	-0.319	-12.061	1.00	0.00	ATOM	926	C	LVS	57	-8.355	-10.144	1.617	1.00	0.00	ATOM	1020	HD1	LEU	63	6.487	-5.604	1.025	1.00	0.00
ATOM	833	N	SER	52	-3.479	-0.182	-9.901	1.00	0.00	ATOM	927	O	LVS	57	-3.197	-11.146	1.895	1.00	0.00	ATOM	1021	HD1	LEU	63	7.937	-6.487	2.992	1.00	0.00
ATOM	834	N	SER	52	-3.479	-0.182	-9.901	1.00	0.00	ATOM	928	N	THR	58	-4.014	-9.714	0.370	1.00	0.00	ATOM	1022	CD2	LEU	63	5.741	-7.580	3.736	1.00	0.00
ATOM	835	N	SER	52	-3.101	-0.622	-9.134	1.00																					

[illegible]

ATOM	1343	CGD	THR	83	-4.464	7.786	-5.633	1.00	0.00	ATOM	1477	H81	ASN	89	-14.820	8.561	-0.042	1.00	0.00	ATOM	1571	O	TVR	95	-10.170	6.352	2.951	1.00	0.00
ATOM	1384	H021	THR	83	-3.664	7.404	-6.333	1.00	0.00	ATOM	1478	CDI	ASN	89	-14.820	8.561	-0.042	1.00	0.00	ATOM	1572	N	TVR	96	-11.743	7.934	3.243	1.00	0.00
ATOM	1385	H022	THR	83	-4.884	8.255	-5.389	1.00	0.00	ATOM	1479	CGI	ASN	89	-12.001	7.796	-0.149	1.00	0.00	ATOM	1573	N	TVR	96	-10.856	7.945	3.032	1.00	0.00
ATOM	1386	H023	THR	83	-8.228	6.656	-6.049	1.00	0.00	ATOM	1480	CDI	ASN	89	-12.001	7.796	-0.149	1.00	0.00	ATOM	1574	CA	TVR	96	-10.856	7.945	3.032	1.00	0.00
ATOM	1387	CA	THR	83	-6.278	6.017	-7.111	1.00	0.00	ATOM	1481	ND2	ASN	89	-13.464	6.135	-0.609	1.00	0.00	ATOM	1575	HA	TVR	96	-10.140	8.795	2.268	1.00	0.00
ATOM	1388	N	ASN	84	-4.333	4.690	-3.766	1.00	0.00	ATOM	1482	ND3	ASN	89	-12.769	5.467	-0.377	1.00	0.00	ATOM	1576	CB	TVR	96	-11.579	10.321	2.712	1.00	0.00
ATOM	1389	N	ASN	84	-4.333	4.690	-3.766	1.00	0.00	ATOM	1483	CD22	ASN	89	-15.348	5.910	-0.912	1.00	0.00	ATOM	1577	H81	TVR	96	-12.301	10.073	2.027	1.00	0.00
ATOM	1390	HN	ASN	84	-5.550	4.470	-4.476	1.00	0.00	ATOM	1484	CD22	ASN	89	-15.348	5.910	-0.912	1.00	0.00	ATOM	1578	H82	TVR	96	-12.001	10.745	3.611	1.00	0.00
ATOM	1391	CA	ASN	84	-7.933	3.987	-4.190	1.00	0.00	ATOM	1485	O	ASN	89	-15.701	10.222	-2.272	1.00	0.00	ATOM	1579	H82	TVR	96	-10.257	11.319	0.759	1.00	0.00
ATOM	1392	CA	ASN	84	-7.822	4.381	-3.153	1.00	0.00	ATOM	1486	N	ALA	90	-16.997	8.680	-3.272	1.00	0.00	ATOM	1580	CDI	TVR	96	-10.524	10.326	0.131	1.00	0.00
ATOM	1393	HA	ASN	84	-6.457	2.744	-4.521	1.00	0.00	ATOM	1487	HN	ALA	90	-17.141	7.728	-3.456	1.00	0.00	ATOM	1581	H81	TVR	96	-10.364	12.672	2.745	1.00	0.00
ATOM	1394	H81	ASN	84	-4.457	2.484	-4.521	1.00	0.00	ATOM	1488	CA	ALA	90	-17.954	9.655	-3.783	1.00	0.00	ATOM	1582	CD2	TVR	96	-10.714	12.672	3.758	1.00	0.00
ATOM	1395	H82	ASN	84	-4.457	2.484	-4.521	1.00	0.00	ATOM	1489	CB	ALA	90	-19.185	8.945	-4.326	1.00	0.00	ATOM	1583	H02	TVR	96	-10.364	12.672	3.758	1.00	0.00
ATOM	1396	CG	ASN	84	-4.464	1.707	-4.762	1.00	0.00	ATOM	1490	CB	ALA	90	-19.185	8.945	-4.326	1.00	0.00	ATOM	1584	HE1	TVR	96	-9.130	11.953	0.159	1.00	0.00
ATOM	1397	ODI	ASN	84	-4.959	2.282	-5.218	1.00	0.00	ATOM	1491	H81	ALA	90	-19.128	7.944	-3.926	1.00	0.00	ATOM	1585	HE2	TVR	96	-9.576	13.501	2.152	1.00	0.00
ATOM	1398	ODI	ASN	84	-4.959	2.282	-5.218	1.00	0.00	ATOM	1492	H82	ALA	90	-20.072	9.490	-4.035	1.00	0.00	ATOM	1586	CE2	TVR	96	-9.312	14.320	2.701	1.00	0.00
ATOM	1399	H021							ATOM	1493	H83	ALA	90	-18.356	10.662	-2.705	1.00	0.00	ATOM	1587	HE2	TVR	96	-9.312	14.320	2.701	1.00	0.00	
ATOM	1400	H022							ATOM	1494	O	ASN	89	-18.657	10.179	-1.487	1.00	0.00	ATOM	1588	CE2	TVR	96	-9.312	14.320	2.701	1.00	0.00	
ATOM	1401	C	ASN	84	-8.670	4.212	-3.201	1.00	0.00	ATOM	1495	N	PRO	91	-19.087	11.013	-0.381	1.00	0.00	ATOM	1589	OH	TVR	96	-8.347	14.282	0.265	1.00	0.00
ATOM	1402	O	ASN	84	-9.656	4.879	-3.513	1.00	0.00	ATOM	1496	N	PRO	91	-19.087	11.013	-0.381	1.00	0.00	ATOM	1590	OH	TVR	96	-8.347	14.282	0.265	1.00	0.00
ATOM	1403	N	CYS	85	-8.520	3.657	-0.303	1.00	0.00	ATOM	1497	CA	PRO	91	-19.505	11.951	0.237	1.00	0.00	ATOM	1591	C	TVR	96	-10.009	9.957	-0.946	1.00	0.00
ATOM	1404	N	CYS	85	-8.520	3.657	-0.303	1.00	0.00	ATOM	1498	HA	PRO	91	-20.176	10.140	-0.237	1.00	0.00	ATOM	1592	O	TVR	96	-8.884	9.764	4.378	1.00	0.00
ATOM	1405	CA	CYS	85	-10.414	3.280	-1.276	1.00	0.00	ATOM	1499	CB	PRO	91	-20.176	10.140	-0.237	1.00	0.00	ATOM	1593	N	LVS	97	-10.593	8.886	5.408	1.00	0.00
ATOM	1406	HA	CYS	85	-10.414	3.280	-1.276	1.00	0.00	ATOM	1501	H82	PRO	91	-20.115	8.730	0.022	1.00	0.00	ATOM	1594	HN	LVS	97	-11.496	8.503	5.443	1.00	0.00
ATOM	1407	HB1	CYS	85	-9.928	3.329	1.109	1.00	0.00	ATOM	1502	H83	PRO	91	-19.704	8.730	0.022	1.00	0.00	ATOM	1595	HN	LVS	97	-9.217	9.050	6.771	1.00	0.00
ATOM	1408	HB1	CYS	85	-9.928	3.329	1.109	1.00	0.00	ATOM	1503	H82	PRO	91	-19.704	8.730	0.022	1.00	0.00	ATOM	1596	HN	LVS	97	-9.217	9.050	6.771	1.00	0.00
ATOM	1409	HB2	CYS	85	-8.132	3.724	0.665	1.00	0.00	ATOM	1504	H01	PRO	91	-18.679	8.764	-1.094	1.00	0.00	ATOM	1597	CB	LVS	97	-10.960	8.901	7.898	1.00	0.00
ATOM	1410	HB2	CYS	85	-8.132	3.724	0.665	1.00	0.00	ATOM	1505	H02	PRO	91	-18.679	8.764	-1.094	1.00	0.00	ATOM	1598	HB1	LVS	97	-11.380	7.906	7.859	1.00	0.00
ATOM	1411	HG	CYS	85	-9.922	0.955	-0.022	1.00	0.00	ATOM	1506	C	PRO	91	-18.998	8.133	-1.819	1.00	0.00	ATOM	1599	HB2	LVS	97	-10.457	9.033	8.845	1.00	0.00
ATOM	1412	C	CYS	85	-9.973	5.278	-0.759	1.00	0.00	ATOM	1507	H02	PRO	91	-18.998	8.133	-1.819	1.00	0.00	ATOM	1600	CG	LVS	97	-12.100	9.903	7.820	1.00	0.00
ATOM	1413	O	CYS	85	-10.996	5.613	-0.398	1.00	0.00	ATOM	1508	C	PRO	91	-17.976	11.268	0.633	1.00	0.00	ATOM	1601	H03	LVS	97	-11.710	10.845	7.473	1.00	0.00
ATOM	1414	N	LVS	86	-8.898	6.150	-0.993	1.00	0.00	ATOM	1509	O	PRO	91	-18.242	11.671	1.766	1.00	0.00	ATOM	1602	CG	LVS	97	-12.756	10.107	9.176	1.00	0.00
ATOM	1415	CA	LVS	86	-8.021	5.820	-1.201	1.00	0.00	ATOM	1510	N	GLU	92	-16.734	11.007	0.234	1.00	0.00	ATOM	1603	CG	LVS	97	-12.756	10.107	9.176	1.00	0.00
ATOM	1416	CA	LVS	86	-8.021	5.820	-1.201	1.00	0.00	ATOM	1511	N	GLU	92	-16.734	11.007	0.234	1.00	0.00	ATOM	1604	HD1	LVS	97	-13.665	10.674	9.042	1.00	0.00
ATOM	1417	HA	LVS	86	-9.725	7.741	-0.029	1.00	0.00	ATOM	1512	CA	GLU	92	-15.586	11.571	-0.174	1.00	0.00	ATOM	1605	HD2	LVS	97	-12.990	9.142	9.601	1.00	0.00
ATOM	1418	CB	LVS	86	-7.758	8.290	-0.623	1.00	0.00	ATOM	1513	HA	GLU	92	-14.728	10.745	0.654	1.00	0.00	ATOM	1606	HE1	LVS	97	-11.552	10.157	13.131	1.00	0.00
ATOM	1419	HB1	LVS	86	-7.355	7.984	-0.330	1.00	0.00	ATOM	1514	CB	GLU	92	-15.340	12.658	1.408	1.00	0.00	ATOM	1607	HE2	LVS	97	-12.411	12.111	10.629	1.00	0.00
ATOM	1420	HB2	LVS	86	-7.078	7.990	-0.147	1.00	0.00	ATOM	1515	HB1	GLU	92	-14.454	12.750	2.020	1.00	0.00	ATOM	1608	HE2	LVS	97	-12.990	9.142	9.601	1.00	0.00
ATOM	1421	H01	LVS	86	-6.858	10.097	0.322	1.00	0.00	ATOM	1516	HB2	GLU	92	-16.183	13.062	1.949	1.00	0.00	ATOM	1609	HE2	LVS	97	-11.552	10.157	13.131	1.00	0.00
ATOM	1422	H01	LVS	86	-6.858	10.097	0.322	1.00	0.00	ATOM	1517	C	GLU	92	-15.586	11.571	-0.174	1.00	0.00	ATOM	1610	HE2	LVS	97	-12.411	12.111	10.629	1.00	0.00
ATOM	1423	H02	LVS	86	-7.625	10.178	0.356	1.00	0.00	ATOM	1518	H02	GLU	92	-15.963	14.125	0.021	1.00	0.00	ATOM	1611	H22	LVS	97	-12.672	12.011	11.646	1.00	0.00
ATOM	1424	CG	LVS	86	-6.832	10.424	-1.636	1.00	0.00	ATOM	1519	H02	GLU	92	-15.963	14.125	0.021	1.00	0.00	ATOM	1612	H22	LVS	97	-12.672	12.011	11.646	1.00	0.00
ATOM	1425	HB1	LVS	86	-7.437	11.020	-2.334	1.00	0.00	ATOM	1520	CG	GLU	92	-13.118	14.235	-0.775	1.00	0.00	ATOM	1613	C	LVS	97	-8.816	8.395	7.189	1.00	0.00
ATOM	1426	HB1	LVS	86	-6.363	9.633	-2.147	1.00	0.00	ATOM	1521	HB2	GLU	92	-13.118	14.235	-0.775	1.00	0.00	ATOM	1614	O	LVS	97	-7.664	8.395	7.189	1.00	0.00
ATOM	1427	CG	LVS	86	-6.363	9.633	-2.147	1.00	0.00	ATOM	1522	HB2	GLU	92	-13.118	14.235	-0.775	1.00	0.00	ATOM	1615	N	CYS	98	-9.167	6.753	6.861	1.00	0.00
ATOM	1428	HB1	LVS	86	-6.744	10.970	0.090	1.00	0.00	ATOM	1523	CA	GLU	92	-15.843	15.021	2.436	1.00	0.00	ATOM	1616	HN	CYS	98	-10.105	6.529	6.684	1.00	0.00
ATOM	1429	HB2	LVS	86	-6.276	12.728	-1.927	1.00	0.00	ATOM	1524	O	GLU	92	-15.843	15.021	2.436	1.00	0.00	ATOM	1617	HA	CYS	98	-9.202	6.771	7.039	1.00	0.00
ATOM	1430	N	LVS	86	-6.207	13.425	-0.041	1.00	0.00	ATOM	1525	N	GLU	92	-15.843	15.021	2.436	1.00	0.00	ATOM	1618	HA	CYS	98	-9.202	6.771	7.039	1.00	0.00
ATOM	1431	H21	LVS	86	-6.207	13.425	-0.041	1.00	0.00	ATOM	1526	HN	GLU	92	-15.843	15.021	2.436	1.00	0.00	ATOM	1619	CB	CYS	98	-8.816	8.395			

[illegible]

	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2
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1947	HR2 LVS	118	4.322	10.506	-5.1227	1.00	0.00
ATOM	1948 C	118	4.021	10.506	-5.1227	1.00	0.00
ATOM	1949 HQ2 LVS	118	3.175	10.140	-6.531	1.00	0.00
ATOM	1950 HQ1 LVS	118	3.077	11.585	-5.522	1.00	0.00
ATOM	1951 C	118	1.642	10.081	-5.053	1.00	0.00
ATOM	1952 HD1 LVS	118	1.422	9.100	-5.449	1.00	0.00
ATOM	1953 HD2 LVS	118	1.422	9.100	-5.449	1.00	0.00
ATOM	1954 C	118	0.827	10.084	-4.374	1.00	0.00
ATOM	1955 HZ1 LVS	118	0.925	11.347	-4.666	1.00	0.00
ATOM	1956 HZ2 LVS	118	1.048	11.932	-5.942	1.00	0.00
ATOM	1957 HZ3 LVS	118	0.324	10.143	-6.543	1.00	0.00
ATOM	1958 HZ1 LVS	118	0.734	9.558	-6.180	1.00	0.00
ATOM	1959 HZ2 LVS	118	0.214	10.234	-7.408	1.00	0.00
ATOM	1960 HZ3 LVS	118	1.097	11.099	-6.778	1.00	0.00
ATOM	1961 C	118	4.484	10.352	-3.687	1.00	0.00
ATOM	1962 OT1 LVS	118	4.765	11.715	-3.761	1.00	0.00
ATOM	1963 OT2 LVS	118	4.903	11.986	-2.445	1.00	0.00
END							

Atomic Structure Coordinates of the
P/CAF Bromodomain/Acetyl-Histamine
Complex

1

251	HE2	TVR	15	9.275	-	8.431	2.377	0.00	0.00	BpD	ATOM	347	HG23	TLR	21	1.319	-	12.844	-9.465	1.00	0.00	BpD	ATOM	441	HE1	LVS	26	-0.1310		
BpD	ATOM	254	CV	11.284	-	8.633	2.603	1.00	0.00	BpD	ATOM	348	HG23	TLR	21	1.073	-	12.885	-9.884	1.00	0.00	BpD	ATOM	442	HE1	LVS	26	-0.358		
BpD	ATOM	255	CV	10.908	-	7.915	3.053	1.00	0.00	BpD	ATOM	349	CU	TLR	21	3.222	-	13.461	-8.179	1.00	0.00	BpD	ATOM	443	HE2	LVS	26	-4.673		
BpD	ATOM	256	HH	TVR	15	6.140	-0.427	1.00	0.00	BpD	ATOM	350	HD11	TLR	21	3.805	-	12.749	-10.120	1.00	0.00	BpD	ATOM	444	C	LVS	38	-5.762		
BpD	ATOM	257	C	TVR	15	10.859	-	5.235	-0.338	1.00	0.00	BpD	ATOM	351	HD12	TLR	21	2.624	-	11.073	-5.468	1.00	0.00	BpD	ATOM	445	C	LVS	38	-4.315
BpD	ATOM	258	N	SR	16	6.370	-0.717	1.00	0.00	BpD	ATOM	352	HD13	TLR	21	1.965	-	10.411	-4.731	1.00	0.00	BpD	ATOM	446	HN	SR	27	-6.104		
BpD	ATOM	259	N	SR	16	11.641	-	6.331	-0.717	1.00	0.00	BpD	ATOM	353	C	TLR	21	0.869	-	12.109	-4.933	1.00	0.00	BpD	ATOM	448	C	LVS	27	-5.204
BpD	ATOM	260	HN	SR	16	9.361	-1.044	1.00	0.00	BpD	ATOM	354	C	TLR	21	0.869	-	12.109	-4.933	1.00	0.00	BpD	ATOM	448	C	LVS	27	-5.204		
BpD	ATOM	261	HA	SR	16	11.249	-	9.361	-1.074	1.00	0.00	BpD	ATOM	355	N	LEU	22	2.433	-	13.257	-4.516	1.00	0.00	BpD	ATOM	449	HA	SR	27	-6.044
BpD	ATOM	262	HA	SR	16	11.148	-	8.408	-2.034	1.00	0.00	BpD	ATOM	356	HN	LEU	22	3.325	-	13.100	-5.091	1.00	0.00	BpD	ATOM	450	C	SR	27	-4.532
BpD	ATOM	263	HA	SR	16	12.315	-	8.284	-2.957	1.00	0.00	BpD	ATOM	357	HN	LEU	22	1.648	-	14.553	-4.976	1.00	0.00	BpD	ATOM	451	H1	SR	27	-3.029
BpD	ATOM	264	HB2	SR	16	13.227	-	7.807	-3.429	1.00	0.00	BpD	ATOM	358	CB	LEU	22	2.451	-	15.341	-4.814	1.00	0.00	BpD	ATOM	452	HB2	SR	27	-4.397
BpD	ATOM	265	HB2	SR	16	11.892	-	7.465	-4.197	1.00	0.00	BpD	ATOM	360	HB1	LEU	22	3.352	-	14.492	-6.351	1.00	0.00	BpD	ATOM	454	HB	SR	27	-3.746
BpD	ATOM	267	HB	SR	16	12.601	-	7.996	-4.462	1.00	0.00	BpD	ATOM	361	HB2	LEU	22	2.728	-	15.300	-6.606	1.00	0.00	BpD	ATOM	455	C	SR	27	-5.591
BpD	ATOM	268	C	SR	16	9.909	-	6.556	-3.483	1.00	0.00	BpD	ATOM	362	CU	LEU	22	1.722	-	13.361	-3.950	1.00	0.00	BpD	ATOM	456	C	SR	27	-5.962
BpD	ATOM	269	C	SR	16	9.082	-	7.084	-3.486	1.00	0.00	BpD	ATOM	363	HEU	LEU	22	2.718	-	14.431	-2.767	1.00	0.00	BpD	ATOM	457	N	HIS	28	-5.477
BpD	ATOM	270	HN	THR	17	10.436	-	6.362	-6.437	1.00	0.00	BpD	ATOM	365	HD11	LEU	22	2.220	-	11.418	-2.788	1.00	0.00	BpD	ATOM	459	C	NIS	28	-5.863
BpD	ATOM	271	HN	THR	17	10.436	-	6.362	-6.437	1.00	0.00	BpD	ATOM	365	HD11	LEU	22	2.220	-	11.418	-2.788	1.00	0.00	BpD	ATOM	459	C	NIS	28	-5.863
BpD	ATOM	272	CA	THR	17	8.514	-	6.314	-7.419	1.00	0.00	BpD	ATOM	366	HD12	LEU	22	3.601	-	12.137	-0.946	1.00	0.00	BpD	ATOM	460	HA	HIS	28	-5.597
BpD	ATOM	273	HA	THR	17	8.318	-	6.898	-6.432	1.00	0.00	BpD	ATOM	367	HD13	LEU	22	2.845	-	13.142	-0.497	1.00	0.00	BpD	ATOM	461	C	HIS	28	-5.125
BpD	ATOM	274	CB	THR	17	8.656	-	5.361	-6.074	1.00	0.00	BpD	ATOM	368	CD2	LEU	22	0.507	-	11.076	-0.217	1.00	0.00	BpD	ATOM	462	H1	HIS	28	-4.073
BpD	ATOM	275	CB	THR	17	9.659	-	6.222	-5.198	1.00	0.00	BpD	ATOM	369	CD1	LEU	22	0.127	-	11.308	-0.210	1.00	0.00	BpD	ATOM	463	H2	HIS	28	-5.263
BpD	ATOM	276	HN	SR	17	9.569	-	6.222	-5.198	1.00	0.00	BpD	ATOM	370	CD1	LEU	22	-0.700	-	11.308	-0.210	1.00	0.00	BpD	ATOM	464	H2	HIS	28	-5.263
BpD	ATOM	277	HO1	THR	17	10.436	-	6.401	-5.918	1.00	0.00	BpD	ATOM	371	HD23	LEU	22	0.790	-	10.884	-1.505	1.00	0.00	BpD	ATOM	465	HD1	HIS	28	-5.742
BpD	ATOM	278	CD2	THR	17	7.346	-	6.401	-5.918	1.00	0.00	BpD	ATOM	372	C	LEU	22	1.243	-	11.931	2.081	1.00	0.00	BpD	ATOM	466	HD1	HIS	28	-5.742
BpD	ATOM	279	HG21	THR	17	6.714	-	9.636	-3.915	1.00	0.00	BpD	ATOM	373	O	LEU	22	0.086	-	12.683	1.866	1.00	0.00	BpD	ATOM	467	CD2	HIS	28	-5.760
BpD	ATOM	280	HG22	THR	17	6.845	-	9.636	-3.915	1.00	0.00	BpD	ATOM	374	N	GLN	23	2.201	-	9.754	1.936	1.00	0.00	BpD	ATOM	468	CD2	HIS	28	-5.760
BpD	ATOM	281	HG23	THR	17	6.845	-	9.636	-3.915	1.00	0.00	BpD	ATOM	374	N	GLN	23	2.201	-	9.754	1.936	1.00	0.00	BpD	ATOM	468	CD2	HIS	28	-5.760
BpD	ATOM	282	CA	THR	17	7.356	-	10.384	-3.715	1.00	0.00	BpD	ATOM	376	C	GLN	23	1.941	-	11.556	3.262	1.00	0.00	BpD	ATOM	470	CA	HIS	28	-6.314
BpD	ATOM	283	O	THR	17	6.420	-	4.420	-4.693	1.00	0.00	BpD	ATOM	377	HA	GLN	23	1.628	-	12.044	4.541	1.00	0.00	BpD	ATOM	471	HE2	HIS	28	-6.119
BpD	ATOM	284	N	LEU	18	7.812	-	11.670	-5.754	1.00	0.00	BpD	ATOM	378	CB	GLN	23	3.118	-	10.139	3.189	1.00	0.00	BpD	ATOM	472	HE2	HIS	28	-6.350
BpD	ATOM	285	HN	LEU	18	8.238	-	12.793	-4.464	1.00	0.00	BpD	ATOM	379	HB1	GLN	23	3.720	-	9.536	3.925	1.00	0.00	BpD	ATOM	473	C	HIS	28	-7.364
BpD	ATOM	286	CA	LEU	18	6.286	-	12.412	-3.652	1.00	0.00	BpD	ATOM	380	HB2	GLN	23	2.731	-	12.017	-0.850	1.00	0.00	BpD	ATOM	474	C	HIS	28	-7.979
BpD	ATOM	287	CA	LEU	18	6.286	-	12.412	-3.652	1.00	0.00	BpD	ATOM	380	HB2	GLN	23	2.731	-	12.017	-0.850	1.00	0.00	BpD	ATOM	474	C	HIS	28	-7.979
BpD	ATOM	288	CB	LEU	18	6.911	-	12.412	-3.652	1.00	0.00	BpD	ATOM	382	H31	GLN	23	4.318	-	12.666	-0.128	1.00	0.00	BpD	ATOM	476	HN	GLN	29	-7.404
BpD	ATOM	289	HB1	LEU	18	7.659	-	13.595	-6.015	1.00	0.00	BpD	ATOM	383	H32	GLN	23	4.886	-	13.189	0.947	1.00	0.00	BpD	ATOM	477	CA	GLN	29	-9.397
BpD	ATOM	290	HB2	LEU	18	6.049	-	13.595	-6.015	1.00	0.00	BpD	ATOM	384	C	GLN	23	3.316	-	12.630	0.936	1.00	0.00	BpD	ATOM	478	CA	GLN	29	-9.836
BpD	ATOM	291	CB	LEU	18	7.377	-	13.697	-6.517	1.00	0.00	BpD	ATOM	385	OB1	GLN	23	2.624	-	12.688	-0.487	1.00	0.00	BpD	ATOM	479	C	GLN	29	-9.940
BpD	ATOM	292	CB	LEU	18	9.301	-	13.697	-6.517	1.00	0.00	BpD	ATOM	386	HB2	GLN	23	3.494	-	13.850	1.090	1.00	0.00	BpD	ATOM	480	HB1	GLN	29	-9.485
BpD	ATOM	293	CA	LEU	18	6.966	-	12.408	-8.134	1.00	0.00	BpD	ATOM	388	HE23	GLN	23	3.085	-	13.431	1.561	1.00	0.00	BpD	ATOM	491	C	GLN	29	-8.766
BpD	ATOM	294	HD11	LEU	18	6.966	-	12.408	-8.134	1.00	0.00	BpD	ATOM	388	HE23	GLN	23	3.085	-	13.431	1.561	1.00	0.00	BpD	ATOM	491	C	GLN	29	-8.766
BpD	ATOM	295	HD12	LEU	18	6.667	-	13.654	-8.786	1.00	0.00	BpD	ATOM	389	C	GLN	23	0.655	-	15.138	0.496	1.00	0.00	BpD	ATOM	482	C	GLN	29	-9.294
BpD	ATOM	296	HD13	LEU	18	7.523	-	12.457	-4.157	1.00	0.00	BpD	ATOM	390	C	GLN	23	-0.207	-	15.138	0.496	1.00	0.00	BpD	ATOM	483	H31	GLN	29	-8.707
BpD	ATOM	297	CD2	LEU	18	6.369	-	12.892	-4.951	1.00	0.00	BpD	ATOM	391	N	GLN	24	0.530	-	15.618	1.227	1.00	0.00	BpD	ATOM	484	CD2	GLN	29	-8.660
BpD	ATOM	298	CD2	LEU	18	6.369	-	12.892	-4.951	1.00	0.00	BpD	ATOM	391	N	GLN	24	0.530	-	15.618	1.227	1.00	0.00	BpD	ATOM	484	CD2	GLN	29	-8.660
BpD	ATOM	299	HD23	LEU	18	6.252	-	12.892	-4.951	1.00	0.00	BpD	ATOM	392	CA	GLN	24	-0.622	-	16.093	-0.921	1.00	0.00	BpD	ATOM	485	CA	GLN	29	-10.358
BpD	ATOM	300	HD23	LEU	18	6.252	-	12.892	-4.951	1.00	0.00	BpD	ATOM	392	CA	GLN	24	-0.622	-	16.093	-0.921	1.00	0.00	BpD	ATOM	485	CA	GLN	29	-10.358
BpD	ATOM	301	C	LEU	18	6.722	-	13.086	-2.203	1.00	0.00	BpD	ATOM	394	HA	GLN	24	-0.951	-	16.290	0.971	1.00	0.00	BpD	ATOM	488	HE21	GLN	29	-12.090
BpD	ATOM	302	C	LEU	18	5.989	-	13.947	-2.797	1.00	0.00	BpD	ATOM	395	CB	GLN	24	-0.325	-	16.910	0.737	1.00	0.00	BpD	ATOM	489	HE22	GLN	29	-11.329
BpD	ATOM	303	O	LEU	18	4.869	-	13.584	-0.783	1.00	0.00	BpD	ATOM	396	CB	GLN	24	0.666	-	15.800	0.919	1.00	0.00	BpD	ATOM	490	C	GLN	29	-9.866
BpD	ATOM	304	N	LVS	19	6.926	-	14.012	-0.785	1.00	0.00	BpD	ATOM	397	HB2	GLN	24	-1.038	-	11.332	0.919	1.00	0.00	BpD	ATOM	491	C	GLN	29	-8.165
BpD																														

515	C	PRO	516	C	PRO	517	C	PRO	518	C	PRO	519	C	PRO	520	C	PRO	521	C	PRO	522	C	PRO	523	C	PRO	524	C	PRO	525	C	PRO	526	C	PRO	527	C	PRO	528	C	PRO	529	C	PRO	530	C	PRO	531	C	PRO	532	C	PRO	533	C	PRO	534	C	PRO	535	C	PRO	536	C	PRO	537	C	PRO	538	C	PRO	539	C	PRO	540	C	PRO	541	C	PRO	542	C	PRO	543	C	PRO	544	C	PRO	545	C	PRO	546	C	PRO	547	C	PRO	548	C	PRO	549	C	PRO	550	C	PRO	551	C	PRO	552	C	PRO	553	C	PRO	554	C	PRO	555	C	PRO	556	C	PRO	557	C	PRO	558	C	PRO	559	C	PRO	560	C	PRO	561	C	PRO	562	C	PRO	563	C	PRO	564	C	PRO	565	C	PRO	566	C	PRO	567	C	PRO	568	C	PRO	569	C	PRO	570	C	PRO	571	C	PRO	572	C	PRO	573	C	PRO	574	C	PRO	575	C	PRO	576	C	PRO	577	C	PRO	578	C	PRO	579	C	PRO	580	C	PRO	581	C	PRO	582	C	PRO	583	C	PRO	584	C	PRO	585	C	PRO	586	C	PRO	587	C	PRO	588	C	PRO	589	C	PRO	590	C	PRO	591	C	PRO	592	C	PRO	593	C	PRO	594	C	PRO	595	C	PRO	596	C	PRO	597	C	PRO	598	C	PRO	599	C	PRO	600	C	PRO	601	C	PRO	602	C	PRO	603	C	PRO	604	C	PRO	605	C	PRO	606	C	PRO	607	C	PRO	608	C	PRO	609	C	PRO	610	C	PRO	611	C	PRO	612	C	PRO	613	C	PRO	614	C	PRO	615	C	PRO	616	C	PRO	617	C	PRO	618	C	PRO	619	C	PRO	620	C	PRO	621	C	PRO	622	C	PRO	623	C	PRO	624	C	PRO	625	C	PRO	626	C	PRO	627	C	PRO	628	C	PRO	629	C	PRO	630	C	PRO	631	C	PRO	632	C	PRO	633	C	PRO	634	C	PRO	635	C	PRO	636	C	PRO	637	C	PRO	638	C	PRO	639	C	PRO	640	C	PRO	641	C	PRO	642	C	PRO	643	C	PRO	644	C	PRO	645	C	PRO	646	C	PRO	647	C	PRO	648	C	PRO	649	C	PRO	650	C	PRO	651	C	PRO	652	C	PRO	653	C	PRO	654	C	PRO	655	C	PRO	656	C	PRO	657	C	PRO	658	C	PRO	659	C	PRO	660	C	PRO	661	C	PRO	662	C	PRO	663	C	PRO	664	C	PRO	665	C	PRO	666	C	PRO	667	C	PRO	668	C	PRO	669	C	PRO	670	C	PRO	671	C	PRO	672	C	PRO	673	C	PRO	674	C	PRO	675	C	PRO	676	C	PRO	677	C	PRO	678	C	PRO	679	C	PRO	680	C	PRO	681	C	PRO	682	C	PRO	683	C	PRO	684	C	PRO	685	C	PRO	686	C	PRO	687	C	PRO	688	C	PRO	689	C	PRO	690	C	PRO	691	C	PRO	692	C	PRO	693	C	PRO	694	C	PRO	695	C	PRO	696	C	PRO	697	C	PRO	698	C	PRO	699	C	PRO	700	C	PRO	701	C	PRO	702	C	PRO	703	C	PRO	704	C	PRO	705	C	PRO	706	C	PRO	707	C	PRO	708	C	PRO	709	C	PRO	710	C	PRO	711	C	PRO	712	C	PRO	713	C	PRO	714	C	PRO	715	C	PRO	716	C	PRO	717	C	PRO	718	C	PRO	719	C	PRO	720	C	PRO	721	C	PRO	722	C	PRO	723	C	PRO	724	C	PRO	725	C	PRO	726	C	PRO	727	C	PRO	728	C	PRO	729	C	PRO	730	C	PRO	731	C	PRO	732	C	PRO	733	C	PRO	734	C	PRO	735	C	PRO	736	C	PRO	737	C	PRO	738	C	PRO	739	C	PRO	740	C	PRO	741	C	PRO	742	C	PRO	743	C	PRO	744	C	PRO	745	C	PRO	746	C	PRO	747	C	PRO	748	C	PRO	749	C	PRO	750	C	PRO	751	C	PRO	752	C	PRO	753	C	PRO	754	C	PRO	755	C	PRO	756	C	PRO	757	C	PRO	758	C	PRO	759	C	PRO	760	C	PRO	761	C	PRO	762	C	PRO	763	C	PRO	764	C	PRO	765	C	PRO	766	C	PRO	767	C	PRO	768	C	PRO	769	C	PRO	770	C	PRO	771	C	PRO	772	C	PRO	773	C	PRO	774	C	PRO	775	C	PRO	776	C	PRO	777	C	PRO	778	C	PRO	779	C	PRO	780	C	PRO	781	C	PRO	782	C	PRO	783	C	PRO	784	C	PRO	785	C	PRO	786	C	PRO	787	C	PRO	788	C	PRO	789	C	PRO	790	C	PRO	791	C	PRO	792	C	PRO	793	C	PRO	794	C	PRO	795	C	PRO	796	C	PRO	797	C	PRO	798	C	PRO	799	C	PRO	800	C	PRO	801	C	PRO	802	C	PRO	803	C	PRO	804	C	PRO	805	C	PRO	806	C	PRO	807	C	PRO	808	C	PRO	809	C	PRO	810	C	PRO	811	C	PRO	812	C	PRO	813	C	PRO	814	C	PRO	815	C	PRO	816	C	PRO	817	C	PRO	818	C	PRO	819	C	PRO	820	C	PRO	821	C	PRO	822	C	PRO	823	C	PRO	824	C	PRO	825	C	PRO	826	C	PRO	827	C	PRO	828	C	PRO	829	C	PRO	830	C	PRO	831	C	PRO	832	C	PRO	833	C	PRO	834	C	PRO	835	C	PRO	836	C	PRO	837	C	PRO	838	C	PRO	839	C	PRO	840	C	PRO	841	C	PRO	842	C	PRO	843	C	PRO	844	C	PRO	845	C	PRO	846	C	PRO	847	C	PRO	848	C	PRO	849	C	PRO	850	C	PRO	851	C	PRO	852	C	PRO	853	C	PRO	854	C	PRO	855	C	PRO	856	C	PRO	857	C	PRO	858	C	PRO	859	C	PRO	860	C	PRO	861	C	PRO	862	C	PRO	863	C	PRO	864	C	PRO	865	C	PRO	866	C	PRO	867	C	PRO	868	C	PRO	869	C	PRO	870	C	PRO	871	C	PRO	872	C	PRO	873	C	PRO	874	C	PRO	875	C	PRO	876	C	PRO	877	C	PRO	878	C	PRO	879	C	PRO	880	C	PRO	881	C	PRO	882	C	PRO	883	C	PRO	884	C	PRO	885	C	PRO	886	C	PRO	887	C	PRO	888	C	PRO	889	C	PRO	890	C	PRO	891	C	PRO	892	C	PRO	893	C	PRO	894	C	PRO	895	C	PRO	896	C	PRO	897	C	PRO	898	C	PRO	899	C	PRO	900	C	PRO
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9.152	0.346	1.00	0.00	BFD ATOM	817	HB	ILE	50	-6.001	0.533	-6.586	1.00	0.00	BFD ATOM	911	CA	LEU	56	-3.306	-	5.934	-13.617	1.00	0.00	BFD ATOM	1005	C	GLU	61	3.565	-
9.152	-0.635	1.00	0.00	BFD ATOM	818	COI	ILE	50	-7.818	0.203	-6.111	1.00	0.00	BFD ATOM	912	HA	LEU	56	-2.301	-	3.174	-12.060	1.00	0.00	BFD ATOM	1006	C	GLU	61	4.466	-
9.035	0.436	1.00	0.00	BFD ATOM	819	COI	ILE	50	-8.256	1.790	-5.932	1.00	0.00	BFD ATOM	913	CA	LEU	56	-3.804	-	3.601	-12.782	1.00	0.00	BFD ATOM	1007	N	ARG	62	3.726	-
10.011	-0.286	1.00	0.00	BFD ATOM	820	H02	ILE	50	-8.158	3.224	-5.932	1.00	0.00	BFD ATOM	914	HB	LEU	56	-3.804	-	2.432	-11.937	1.00	0.00	BFD ATOM	1008	N	ARG	62	4.999	-
8.371	-0.344	1.00	0.00	BFD ATOM	821	COI	ILE	50	-8.644	4.113	-5.932	1.00	0.00	BFD ATOM	915	CA	LEU	56	-3.088	-	1.428	-11.937	1.00	0.00	BFD ATOM	1009	CA	ARG	62	5.352	-
7.815	-0.684	1.00	0.00	BFD ATOM	822	H02	ILE	50	-6.289	3.451	-3.962	1.00	0.00	BFD ATOM	916	CA	LEU	56	-3.358	-	1.262	-11.155	1.00	0.00	BFD ATOM	1010	HA	ARG	62	4.807	-
7.250	1.139	1.00	0.00	BFD ATOM	823	H02	ILE	50	-4.694	2.661	-3.929	1.00	0.00	BFD ATOM	917	HB	LEU	56	-3.358	-	0.075	-10.468	1.00	0.00	BFD ATOM	1011	CA	ARG	62	5.753	-
7.981	1.169	1.00	0.00	BFD ATOM	824	COI	ILE	50	-8.324	4.770	-3.344	1.00	0.00	BFD ATOM	918	CA	LEU	56	-3.521	-	0.241	-10.052	1.00	0.00	BFD ATOM	1012	HB	ARG	62	4.091	-
8.495	1.757	1.00	0.00	BFD ATOM	825	H02	ILE	50	-8.330	5.539	-3.406	1.00	0.00	BFD ATOM	919	CA	LEU	56	-2.009	-	0.157	-11.408	1.00	0.00	BFD ATOM	1013	HB	ARG	62	4.991	-
7.923	2.489	1.00	0.00	BFD ATOM	826	H02	ILE	50	-7.674	5.040	-3.719	1.00	0.00	BFD ATOM	920	CA	LEU	56	-4.497	-	1.928	-11.195	1.00	0.00	BFD ATOM	1014	HB	ARG	62	4.852	-
7.704	2.094	1.00	0.00	BFD ATOM	827	H02	ILE	50	-4.490	3.419	-4.553	1.00	0.00	BFD ATOM	921	CA	LEU	56	-1.352	-	0.714	-12.424	1.00	0.00	BFD ATOM	1015	HB	ARG	62	4.494	-
10.827	0.718	1.00	0.00	BFD ATOM	828	H02	ILE	50	-4.504	3.388	-5.909	1.00	0.00	BFD ATOM	922	CA	LEU	56	-1.352	-	1.278	-11.225	1.00	0.00	BFD ATOM	1016	HB	ARG	62	2.826	-
11.444	-0.227	1.00	0.00	BFD ATOM	829	CA	ARG	51	-3.184	4.306	-3.716	1.00	0.00	BFD ATOM	923	CA	LEU	56	-1.144	-	0.738	-10.356	1.00	0.00	BFD ATOM	1017	CA	ARG	62	2.484	-
10.597	1.428	1.00	0.00	BFD ATOM	830	CA	ARG	51	-3.184	2.542	-3.671	1.00	0.00	BFD ATOM	924	CA	LEU	56	-1.175	-	2.356	-11.072	1.00	0.00	BFD ATOM	1018	CA	ARG	62	2.875	-
10.086	2.260	1.00	0.00	BFD ATOM	831	CA	ARG	51	-2.082	2.400	-7.807	1.00	0.00	BFD ATOM	925	CA	LEU	56	-3.305	-	0.058	-12.346	1.00	0.00	BFD ATOM	1019	CA	ARG	62	1.621	-
11.061	0.969	1.00	0.00	BFD ATOM	832	CA	ARG	51	-2.968	2.204	-8.207	1.00	0.00	BFD ATOM	926	CA	LEU	56	-4.717	-	1.585	-11.485	1.00	0.00	BFD ATOM	1020	CA	ARG	62	1.903	-
10.491	1.470	1.00	0.00	BFD ATOM	833	CA	ARG	51	-1.452	2.020	-7.696	1.00	0.00	BFD ATOM	927	CA	LEU	56	-5.261	-	1.125	-11.498	1.00	0.00	BFD ATOM	1021	CA	ARG	62	1.183	-
10.041	2.754	1.00	0.00	BFD ATOM	834	CA	ARG	51	-0.478	2.639	-9.615	1.00	0.00	BFD ATOM	928	CA	LEU	56	-4.634	-	1.678	-15.324	1.00	0.00	BFD ATOM	1022	CA	ARG	62	1.072	-
8.38	3.341	1.00	0.00	BFD ATOM	835	CA	ARG	51	0.048	3.712	-9.704	1.00	0.00	BFD ATOM	929	CA	LEU	56	-4.277	-	0.286	-14.437	1.00	0.00	BFD ATOM	1023	CA	ARG	62	2.359	-
11.516	2.301	1.00	0.00	BFD ATOM	836	CA	ARG	51	-0.399	2.179	-10.108	1.00	0.00	BFD ATOM	930	CA	LEU	56	-6.007	-	3.329	-14.399	1.00	0.00	BFD ATOM	1024	CA	ARG	62	3.018	-
12.185	3.022	1.00	0.00	BFD ATOM	837	CA	ARG	51	0.043	1.139	-9.890	1.00	0.00	BFD ATOM	931	CA	LEU	56	-7.133	-	4.605	-6.247	1.00	0.00	BFD ATOM	1025	CA	ARG	62	6.040	-
12.929	1.120	1.00	0.00	BFD ATOM	838	CA	ARG	51	0.514	2.328	-11.608	1.00	0.00	BFD ATOM	932	CA	LEU	56	-6.203	-	2.255	-10.405	1.00	0.00	BFD ATOM	1026	CA	ARG	62	7.101	-
11.177	0.233	1.00	0.00	BFD ATOM	839	CA	ARG	51	-0.090	1.845	-12.118	1.00	0.00	BFD ATOM	933	CA	LEU	56	-5.383	-	2.569	-10.945	1.00	0.00	BFD ATOM	1027	CA	ARG	62	6.551	-
12.789	1.989	1.00	0.00	BFD ATOM	840	CA	ARG	51	1.923	1.856	-11.889	1.00	0.00	BFD ATOM	934	CA	LEU	56	-7.148	-	2.606	-9.128	1.00	0.00	BFD ATOM	1028	CA	ARG	62	6.731	-
12.730	2.212	1.00	0.00	BFD ATOM	841	CA	ARG	51	2.296	3.780	-12.024	1.00	0.00	BFD ATOM	935	CA	LEU	56	-5.471	-	3.396	-8.339	1.00	0.00	BFD ATOM	1029	CA	ARG	62	7.456	-
11.678	0.602	1.00	0.00	BFD ATOM	842	CA	ARG	51	4.491	4.383	-12.161	1.00	0.00	BFD ATOM	936	CA	LEU	56	-7.210	-	2.771	-8.093	1.00	0.00	BFD ATOM	1030	CA	ARG	62	5.962	-
14.046	-0.132	1.00	0.00	BFD ATOM	843	CA	ARG	51	4.284	3.073	-13.697	1.00	0.00	BFD ATOM	937	CA	LEU	56	-7.354	-	3.840	-7.043	1.00	0.00	BFD ATOM	1031	CA	ARG	62	5.009	-
13.610	1.532	1.00	0.00	BFD ATOM	844	CA	ARG	51	2.206	4.515	-12.715	1.00	0.00	BFD ATOM	938	CA	LEU	56	-6.778	-	4.277	-7.302	1.00	0.00	BFD ATOM	1032	CA	ARG	62	5.780	-
13.739	-1.622	1.00	0.00	BFD ATOM	845	CA	ARG	51	2.779	4.515	-12.715	1.00	0.00	BFD ATOM	939	CA	LEU	56	-8.032	-	2.962	-6.442	1.00	0.00	BFD ATOM	1033	CA	ARG	62	6.429	-
10.631	-0.473	1.00	0.00	BFD ATOM	846	CA	ARG	51	-1.272	5.025	-11.495	1.00	0.00	BFD ATOM	940	CA	LEU	56	-9.133	-	4.754	-5.156	1.00	0.00	BFD ATOM	1034	CA	ARG	62	8.237	-
10.631	-0.473	1.00	0.00	BFD ATOM	847	CA	ARG	51	-1.644	3.723	-12.391	1.00	0.00	BFD ATOM	941	CA	LEU	56	-9.122	-	4.605	-6.247	1.00	0.00	BFD ATOM	1035	CA	ARG	62	8.450	-
9.322	-1.687	1.00	0.00	BFD ATOM	848	CA	ARG	51	-1.843	2.015	-10.473	1.00	0.00	BFD ATOM	942	CA	LEU	56	-3.533	-	3.584	-6.547	1.00	0.00	BFD ATOM	1036	CA	ARG	62	8.685	-
8.718	0.067	1.00	0.00	BFD ATOM	849	CA	ARG	51	-2.010	2.516	-11.553	1.00	0.00	BFD ATOM	943	CA	LEU	56	-3.222	-	4.618	-9.103	1.00	0.00	BFD ATOM	1037	CA	ARG	62	7.150	-
8.718	0.067	1.00	0.00	BFD ATOM	850	CA	ARG	51	-2.010	2.516	-11.553	1.00	0.00	BFD ATOM	944	CA	LEU	56	-3.222	-	4.618	-9.103	1.00	0.00	BFD ATOM	1038	CA	ARG	62	8.354	-
8.718	0.067	1.00	0.00	BFD ATOM	851	CA	ARG	51	-2.010	2.516	-11.553	1.00	0.00	BFD ATOM	945	CA	LEU	56	-3.222	-	4.618	-9.103	1.00	0.00	BFD ATOM	1039	CA	ARG	62	8.354	-
8.718	0.067	1.00	0.00	BFD ATOM	852	CA	ARG	51	-2.010	2.516	-11.553	1.00	0.00	BFD ATOM	946	CA	LEU	56	-3.222	-	4.618	-9.103	1.00	0.00	BFD ATOM	1040	CA	ARG	62	8.354	-
8.718	0.067	1.00	0.00	BFD ATOM	853	CA	ARG	51	-2.010	2.516	-11.553	1.00	0.00	BFD ATOM	947	CA	LEU	56	-3.222	-	4.618	-9.103	1.00	0.00	BFD ATOM	1041	CA	ARG	62	8.354	-
8.718	0.067	1.00	0.00	BFD ATOM	854	CA	ARG	51	-2.010	2.516	-11.553	1.00	0.00	BFD ATOM	948	CA	LEU	56	-3.222	-	4.618	-9.103	1.00	0.00	BFD ATOM	1042	CA	ARG	62	8.354	-
8.718	0.067	1.00	0.00	BFD ATOM	855	CA	ARG	51	-2.010	2.516	-11.553	1.00	0.00	BFD ATOM	949	CA	LEU	56	-3.222	-	4.618	-9.103	1.00	0.00	BFD ATOM	1043	CA	ARG	62	8.354	-
8.718	0.067	1.00	0.00	BFD ATOM	856	CA	ARG	51	-2.010	2.516	-11.553	1.00	0.00	BFD ATOM	950	CA	LEU	56	-3.222	-	4.618	-9.103	1.00	0.00	BFD ATOM	1044	CA	ARG	62	8.354	-
8.718	0.067	1.00	0.00	BFD ATOM	857	CA	ARG	51	-2.010	2.516	-11.553	1.00	0.00	BFD ATOM	951	CA	LEU	56	-3.222	-	4.618	-9.103	1.00	0.00	BFD ATOM	1045	CA	ARG	62	8.354	-
8.718	0.067	1.00	0.00	BFD ATOM	858	CA	ARG	51	-2.010	2.516	-11.553	1.00	0.00	BFD ATOM	952	CA	LEU	56	-3.222	-	4.618	-9.103	1.00	0.00	BFD ATOM	1046	CA	ARG	62	8.354	-
8.718	0.067	1.00	0.00	BFD ATOM	859	CA	ARG	51	-2.010	2.516	-11.553	1.00	0.00	BFD ATOM	953	CA	LEU	56	-3.222	-	4.618	-9.103	1.00	0.00	BFD ATOM	1047	CA	ARG	62	8.354	-
8.718	0.067	1.00	0.00	BFD ATOM	860	CA	ARG	51	-2.010	2.516	-11.553	1.00	0.00	BFD ATOM	954	CA	LEU	56	-3.222	-	4.618	-9.103	1.00	0.00	BFD ATOM	1048	CA	ARG	62	8.354	-
8.718	0.067	1.00	0.00	BFD ATOM	861	CA	ARG	51	-2.010	2.516	-11.553	1.00	0.00	BFD ATOM	955	CA	LEU	56	-3.222	-	4.618	-9.103	1.00	0.00	BFD ATOM	1049	CA	ARG	62	8.354	-
8.718	0.067	1.00	0.00	BFD ATOM	862	CA	ARG	51	-2.010	2.516	-11.553	1.00	0.00	BFD ATOM	956	CA	LEU	56	-3.222	-	4.618	-9.103	1.00	0.00	BFD ATOM	1050	CA	ARG	62	8.354	-

6.328	-9.898	1.00	0.00	BFD ATOM	1099	NE	ARG	66	15	162	-	3.727	2.548	1.00	0.00	BFD ATOM	1193	HE1	LVS	71	14.024	6.842	2.049	1.00	0.00	BFD ATOM	1287	C	ALA	76	2.240
5.351	-10.237	1.00	0.00	BFD ATOM	1100	CI	ARG	66	15	688	-	4.084	1.699	1.00	0.00	BFD ATOM	1194	HE2	LVS	71	14.024	4.601	1.147	1.00	0.00	BFD ATOM	1288	O	ALA	76	1.211
5.265	-11.059	1.00	0.00	BFD ATOM	1101	CE	ARG	66	15	688	-	4.084	1.699	1.00	0.00	BFD ATOM	1195	HE3	LVS	71	14.024	5.026	1.666	1.00	0.00	BFD ATOM	1289	N	ASP	77	2.270
5.407	-9.074	1.00	0.00	BFD ATOM	1102	HA1	ARG	66	14	117	-	2.757	1.000	0.00	0.00	BFD ATOM	1196	HE4	LVS	71	14.024	4.014	-0.044	1.00	0.00	BFD ATOM	1290	HN	ASP	77	3.124
5.407	-7.945	1.00	0.00	BFD ATOM	1103	HA2	ARG	66	14	118	-	3.334	4.558	1.00	0.00	BFD ATOM	1197	HE5	LVS	71	14.024	3.685	-0.394	1.00	0.00	BFD ATOM	1291	HA	ASP	77	0.460
5.378	-7.969	1.00	0.00	BFD ATOM	1104	HA3	ARG	66	14	118	-	4.880	4.058	1.00	0.00	BFD ATOM	1198	HE6	LVS	71	14.024	3.404	-0.765	1.00	0.00	BFD ATOM	1292	CB	ASP	77	1.392
5.334	-9.037	1.00	0.00	BFD ATOM	1105	HA4	ARG	66	17	624	-	3.533	6.331	1.00	0.00	BFD ATOM	1199	C	LVS	71	9.041	3.534	-2.283	1.00	0.00	BFD ATOM	1293	CB	ASP	77	2.196
5.377	-9.861	1.00	0.00	BFD ATOM	1106	HA5	ARG	66	17	624	-	3.160	-0.231	1.00	0.00	BFD ATOM	1200	N	LVS	72	9.041	2.817	-2.334	1.00	0.00	BFD ATOM	1294	HA2	ASP	77	0.921
5.377	-9.861	1.00	0.00	BFD ATOM	1107	HA6	ARG	66	17	624	-	2.529	-0.166	1.00	0.00	BFD ATOM	1201	N	LVS	72	9.041	3.128	-2.776	1.00	0.00	BFD ATOM	1295	HA3	ASP	77	1.817
5.377	-9.861	1.00	0.00	BFD ATOM	1108	HA7	ARG	66	10	658	-	4.898	0.211	1.00	0.00	BFD ATOM	1202	HN	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1296	CB	ASP	77	1.817
5.377	-9.861	1.00	0.00	BFD ATOM	1109	HA8	ARG	66	10	658	-	4.898	0.211	1.00	0.00	BFD ATOM	1203	HN	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1297	CB	ASP	77	1.817
5.377	-9.861	1.00	0.00	BFD ATOM	1110	HA9	ARG	66	10	658	-	4.898	0.211	1.00	0.00	BFD ATOM	1204	HA	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1298	CB	ASP	77	1.817
5.377	-9.861	1.00	0.00	BFD ATOM	1111	HA10	ARG	66	7	836	-	5.201	0.351	1.00	0.00	BFD ATOM	1205	CA	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1299	O	ASP	77	-0.950
5.377	-9.861	1.00	0.00	BFD ATOM	1112	HA11	ARG	66	7	836	-	6.884	0.547	1.00	0.00	BFD ATOM	1206	CA	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1300	N	LEU	78	0.970
5.377	-9.861	1.00	0.00	BFD ATOM	1113	HA12	ARG	66	7	836	-	4.818	1.255	1.00	0.00	BFD ATOM	1207	HE2	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1301	N	LEU	78	1.948
5.377	-9.861	1.00	0.00	BFD ATOM	1114	HA13	ARG	66	7	836	-	7.216	0.324	1.00	0.00	BFD ATOM	1208	HE3	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1302	N	LEU	78	1.948
5.377	-9.861	1.00	0.00	BFD ATOM	1115	HA14	ARG	66	7	836	-	6.950	1.687	1.00	0.00	BFD ATOM	1209	HE4	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1303	N	LEU	78	1.948
5.377	-9.861	1.00	0.00	BFD ATOM	1116	HA15	ARG	66	7	836	-	6.950	1.687	1.00	0.00	BFD ATOM	1210	HE5	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1304	N	LEU	78	1.948
5.377	-9.861	1.00	0.00	BFD ATOM	1117	HA16	ARG	66	7	836	-	7.895	1.515	1.00	0.00	BFD ATOM	1211	CD1	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1305	C	LEU	78	-0.493
5.377	-9.861	1.00	0.00	BFD ATOM	1118	CD2	LVS	67	7	713	-	7.004	3.027	1.00	0.00	BFD ATOM	1212	CD2	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1306	C	LEU	78	-0.493
5.377	-9.861	1.00	0.00	BFD ATOM	1119	CD3	LVS	67	6	132	-	8.128	3.147	1.00	0.00	BFD ATOM	1213	CD3	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1307	H2	LEU	78	2.212
5.377	-9.861	1.00	0.00	BFD ATOM	1120	CD4	LVS	67	6	132	-	8.128	3.147	1.00	0.00	BFD ATOM	1214	CE	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1308	H2	LEU	78	2.212
5.377	-9.861	1.00	0.00	BFD ATOM	1121	CD5	LVS	67	6	132	-	8.128	3.147	1.00	0.00	BFD ATOM	1215	HE1	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1309	H2	LEU	78	2.212
5.377	-9.861	1.00	0.00	BFD ATOM	1122	CD6	LVS	67	6	132	-	8.128	3.147	1.00	0.00	BFD ATOM	1216	HE2	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1310	H2	LEU	78	2.212
5.377	-9.861	1.00	0.00	BFD ATOM	1123	CD7	LVS	67	6	132	-	8.128	3.147	1.00	0.00	BFD ATOM	1217	HE3	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1311	H2	LEU	78	2.212
5.377	-9.861	1.00	0.00	BFD ATOM	1124	CD8	LVS	67	6	132	-	8.128	3.147	1.00	0.00	BFD ATOM	1218	HE4	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1312	H2	LEU	78	2.212
5.377	-9.861	1.00	0.00	BFD ATOM	1125	CD9	LVS	67	6	132	-	8.128	3.147	1.00	0.00	BFD ATOM	1219	HE5	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1313	H2	LEU	78	2.212
5.377	-9.861	1.00	0.00	BFD ATOM	1126	CD10	LVS	67	6	132	-	8.128	3.147	1.00	0.00	BFD ATOM	1220	CD1	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1314	CD2	LEU	78	0.119
5.377	-9.861	1.00	0.00	BFD ATOM	1127	CD11	LVS	67	6	132	-	8.128	3.147	1.00	0.00	BFD ATOM	1221	CD2	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1315	CD2	LEU	78	0.119
5.377	-9.861	1.00	0.00	BFD ATOM	1128	CD12	LVS	67	6	132	-	8.128	3.147	1.00	0.00	BFD ATOM	1222	CD3	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1316	CD2	LEU	78	0.119
5.377	-9.861	1.00	0.00	BFD ATOM	1129	CD13	LVS	67	6	132	-	8.128	3.147	1.00	0.00	BFD ATOM	1223	CD4	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1317	CD2	LEU	78	0.119
5.377	-9.861	1.00	0.00	BFD ATOM	1130	CD14	LVS	67	6	132	-	8.128	3.147	1.00	0.00	BFD ATOM	1224	CD5	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1318	C	LEU	78	-0.253
5.377	-9.861	1.00	0.00	BFD ATOM	1131	CD15	LVS	67	6	132	-	8.128	3.147	1.00	0.00	BFD ATOM	1225	CD6	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1319	C	LEU	78	-0.253
5.377	-9.861	1.00	0.00	BFD ATOM	1132	CD16	LVS	67	6	132	-	8.128	3.147	1.00	0.00	BFD ATOM	1226	CD7	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1320	N	GLN	79	0.411
5.377	-9.861	1.00	0.00	BFD ATOM	1133	CD17	LVS	67	6	132	-	8.128	3.147	1.00	0.00	BFD ATOM	1227	CD8	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1321	N	GLN	79	0.411
5.377	-9.861	1.00	0.00	BFD ATOM	1134	CD18	LVS	67	6	132	-	8.128	3.147	1.00	0.00	BFD ATOM	1228	CD9	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1322	N	GLN	79	0.411
5.377	-9.861	1.00	0.00	BFD ATOM	1135	CD19	LVS	67	6	132	-	8.128	3.147	1.00	0.00	BFD ATOM	1229	CD10	LVS	72	9.933	4.790	-3.018	1.00	0.00	BFD ATOM	1323	N	GLN	79	0.411
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Measurement	Unit	Mean	SD	Median	Range
Age	yr	50.5	10.5	48.0	30-75
Weight	kg	75.5	15.5	70.0	50-110
Height	m	1.75	0.08	1.73	1.55-1.95
BMI	kg/m ²	24.5	4.5	23.0	18.0-35.0
SBP	mmHg	135	15	130	110-160
DBP	mmHg	85	10	80	70-100
HR	beats/min	75	12	72	60-100
ECG					
Normal		10			
Abnormal		90			
Left bundle branch block		5			
Right bundle branch block		10			
Premature ventricular contractions		15			
ST-T wave changes		20			
Atrial fibrillation		5			
Atrial flutter		2			
Sinus bradycardia		3			
Sinus tachycardia		4			
First degree AV block		1			
Second degree AV block		1			
Third degree AV block		1			
Bundle branch block		2			
Premature atrial contractions		12			
Premature junctional contractions		5			
Premature ventricular contractions		18			
ST segment depression		15			
ST segment elevation		10			
T wave inversion		12			
T wave upright		18			
QT interval	ms	380	20	370	340-420
QTc interval	ms	40	10	38	30-50
QTd interval	ms	50	15	45	35-70
QTs interval	ms	60	20	55	40-80
QTt interval	ms	70	25	65	50-100
QTp interval	ms	80	30	75	60-110
QTm interval	ms	90	35	85	70-120
QTn interval	ms	100	40	95	80-130
QTx interval	ms	110	45	105	90-140
QTy interval	ms	120	50	115	100-150
QTz interval	ms	130	55	125	110-160
QTa interval	ms	140	60	135	120-170
QTb interval	ms	150	65	145	130-180
QTc interval	ms	160	70	155	140-190
QTd interval	ms	170	75	165	150-200
QTe interval	ms	180	80	175	160-210
QTf interval	ms	190	85	185	170-220
QTg interval	ms	200	90	195	180-230
QTh interval	ms	210	95	205	190-240
QTi interval	ms	220	100	215	200-250
QTj interval	ms	230	105	225	210-260
QTk interval	ms	240	110	235	220-270
QTL interval	ms	250	115	245	230-280
QTM interval	ms	260	120	255	240-290
QTN interval	ms	270	125	265	250-300
QTO interval	ms	280	130	275	260-310
QTP interval	ms	290	135	285	270-320
QTM interval	ms	300	140	295	280-330
QTN interval	ms	310	145	305	290-340
QTO interval	ms	320	150	315	300-350
QTP interval	ms	330	155	325	310-360
QTM interval	ms	340	160	335	320-370
QTN interval	ms	350	165	345	330-380
QTO interval	ms	360	170	355	340-390
QTP interval	ms	370	175	365	350-400
QTM interval	ms	380	180	375	360-410
QTN interval	ms	390	185	385	370-420
QTO interval	ms	400	190	395	380-430
QTP interval	ms	410	195	405	390-440
QTM interval	ms	420	200	415	400-450
QTN interval	ms	430	205	425	410-460
QTO interval	ms	440	210	435	420-470
QTP interval	ms	450	215	445	430-480
QTM interval	ms	460	220	455	440-490
QTN interval	ms	470	225	465	450-500
QTO interval	ms	480	230	475	460-510
QTP interval	ms	490	235	485	470-520
QTM interval	ms	500	240	495	480-530
QTN interval	ms	510	245	505	490-540
QTO interval	ms	520	250	515	500-550
QTP interval	ms	530	255	525	510-560
QTM interval	ms	540	260	535	520-570
QTN interval	ms	550	265	545	530-580
QTO interval	ms	560	270	555	540-590
QTP interval	ms	570	275	565	550-600
QTM interval	ms	580	280	575	560-610
QTN interval	ms	590	285	585	570-620
QTO interval	ms	600	290	595	580-630
QTP interval	ms	610	295	605	590-640
QTM interval	ms	620	300	615	600-650
QTN interval	ms	630	305	625	610-660
QTO interval	ms	640	310	635	620-670
QTP interval	ms	650	315	645	630-680
QTM interval	ms	660	320	655	640-690
QTN interval	ms	670	325	665	650-700
QTO interval	ms	680	330	675	660-710
QTP interval	ms	690	335	685	670-720
QTM interval	ms	700	340	695	680-730
QTN interval	ms	710	345	705	690-740
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QTP interval	ms	730	355	725	710-760
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QTN interval	ms	750	365	745	730-780
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QTM interval	ms	780	380	775	760-810
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QTP interval	ms	850	415	845	830-880
QTM interval	ms	860	420	855	840-890
QTN interval	ms	870	425	865	850-900
QTO interval	ms	880	430	875	860-910
QTP interval	ms	890	435	885	870-920
QTM interval	ms	900	440	895	880-930
QTN interval	ms	910	445	905	890-940
QTO interval	ms	920	450	915	900-950
QTP interval	ms	930	455	925	910-960
QTM interval	ms	940	460	935	920-970
QTN interval	ms	950	465	945	930-980
QTO interval	ms	960	470	955	940-990
QTP interval	ms	970	475	965	950-1000
QTM interval	ms	980	480	975	960-1010
QTN interval	ms	990	485	985	970-1020
QTO interval	ms	1000	490	995	980-1030

7

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0.086	6.812	1.00	0.00	BxD ATOM	1949	C	ILE	116	6.802
1.751	8.053	1.00	0.00	BxD ATOM	1950	O	ILE	116	7.024
0.544	8.154	1.00	0.00	BxD ATOM	1951	N	ASP	117	6.222
0.544	8.154	1.00	0.00	BxD ATOM	1952	N	ASP	117	6.222
3.453	9.014	1.00	0.00	BxD ATOM	1953	EN	ASP	117	5.905
0.544	8.154	1.00	0.00	BxD ATOM	1954	HA	ASP	117	5.197
1.862	10.275	1.00	0.00	BxD ATOM	1955	CB	ASP	117	4.967
2.585	10.798	1.00	0.00	BxD ATOM	1956	HB1	ASP	117	5.564
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2.053	10.968	1.00	0.00	BxD ATOM	1967	CB	LVS	118	8.636
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3.719	12.295	1.00	0.00	BxD ATOM	1972	HB2	LVS	118	10.477
3.946	13.911	1.00	0.00	BxD ATOM	1973	CD	LVS	118	10.468
4.608	12.327	1.00	0.00	BxD ATOM	1974	HD1	LVS	118	9.208
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4.075	11.613	1.00	0.00	BxD ATOM	1976	CB	LVS	118	10.212
5.425	10.902	1.00	0.00	BxD ATOM	1977	HB2	LVS	118	11.163
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6.458	11.316	1.00	0.00	BxD ATOM	1980	HB2	LVS	118	9.947
7.658	11.096	1.00	0.00	BxD ATOM	1981	HB2	LVS	118	10.454
8.130	11.891	1.00	0.00	BxD ATOM	1982	HB2	LVS	118	
0.130	11.891	1.00	0.00	BxD ATOM	1983	HB2	LVS	118	
0.641	10.802	1.00	0.00	BxD ATOM	1984	OT1	LVS	118	
0.302	12.459	1.00	0.00	BxD ATOM	1985	OT2	LVS	118	
0.302	12.459	1.00	0.00	BxD END					

Structure-based sequence homology alignment of bromodomains

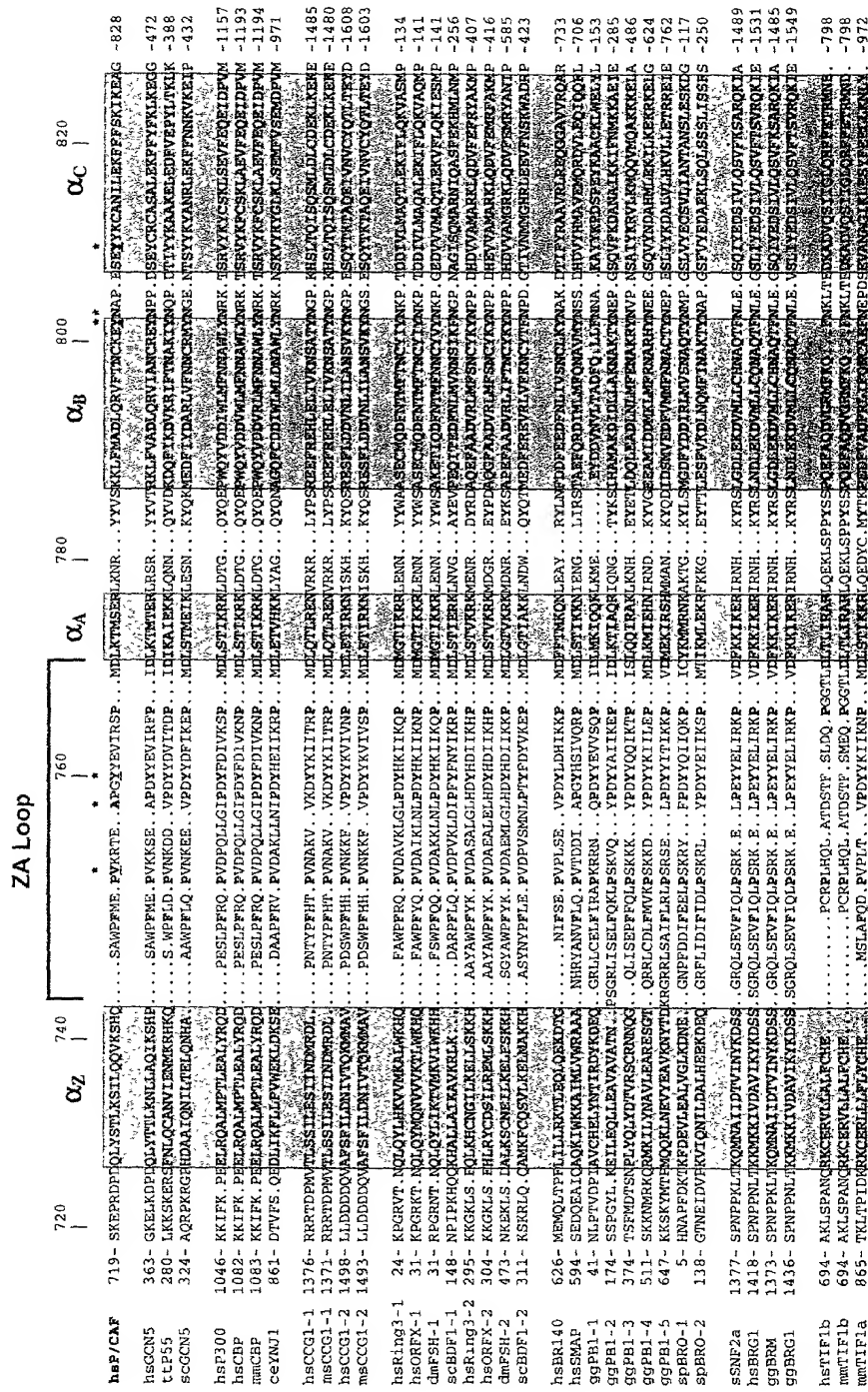


Figure 1

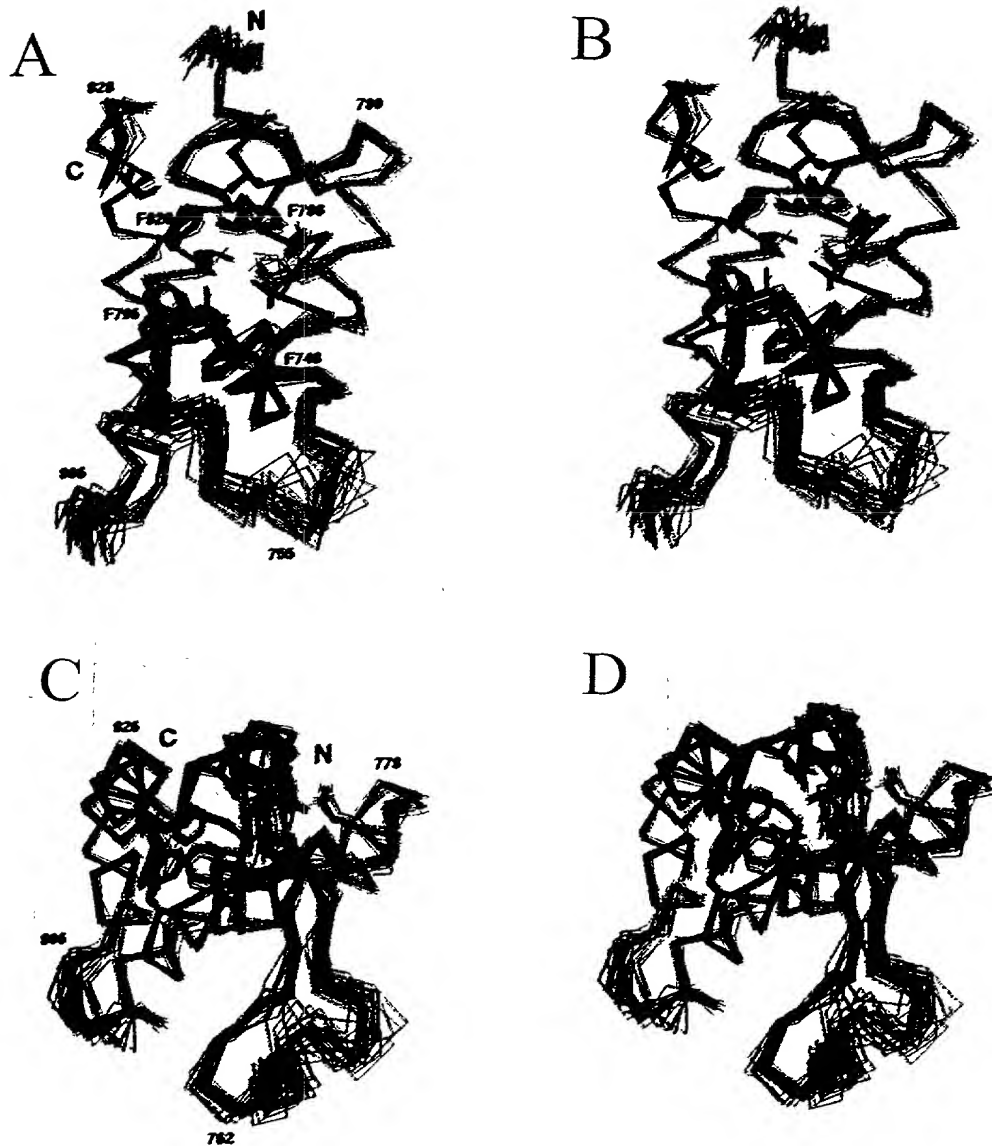


Figure 2A-2D

Three-Dimensional Structure of the P/CAF Bromodomain

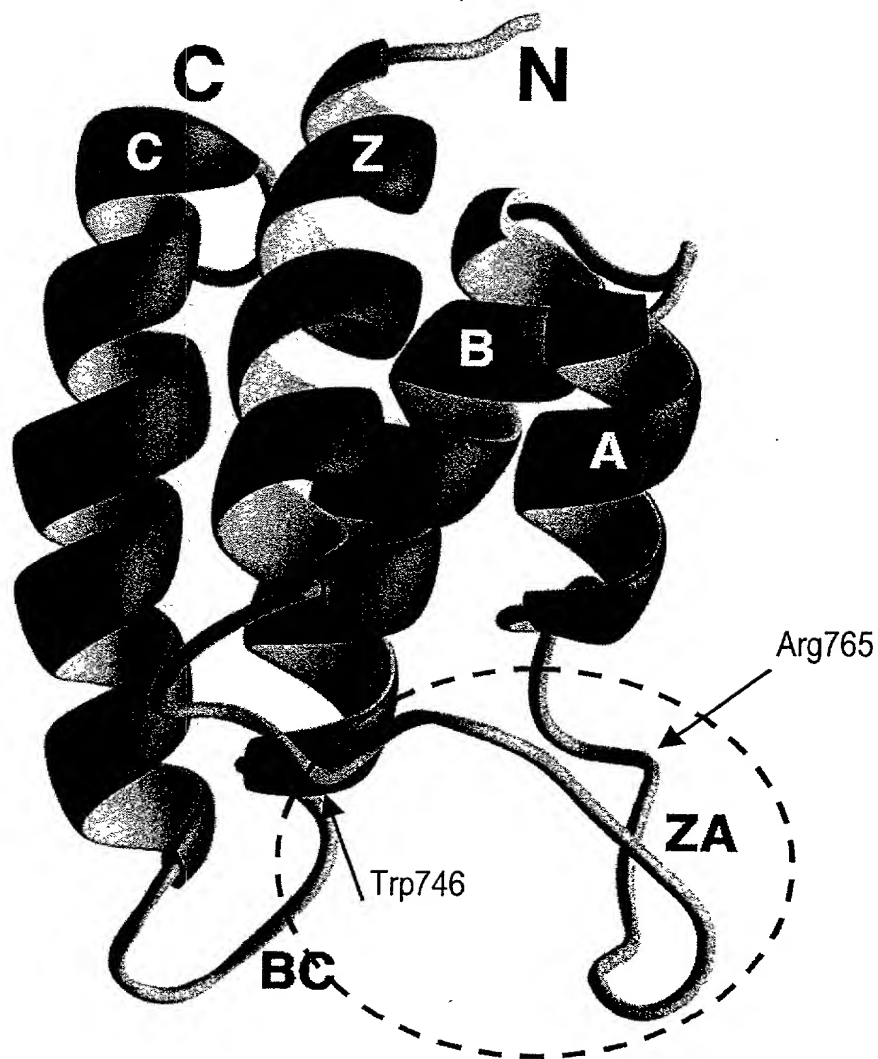


Figure 2E

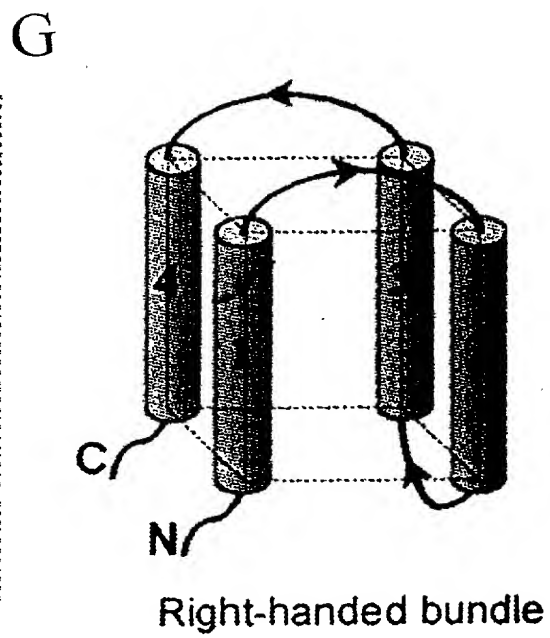
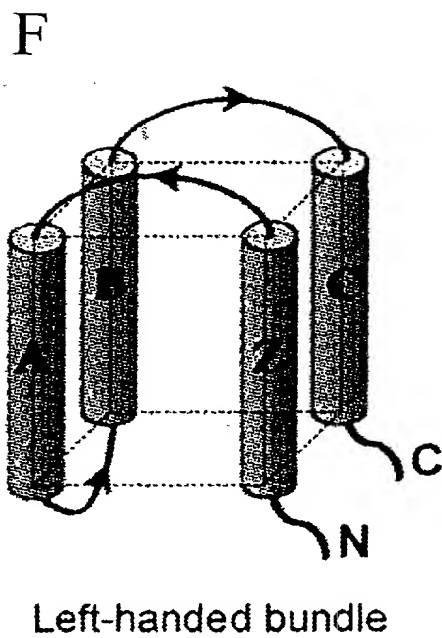


Figure 2F-2G

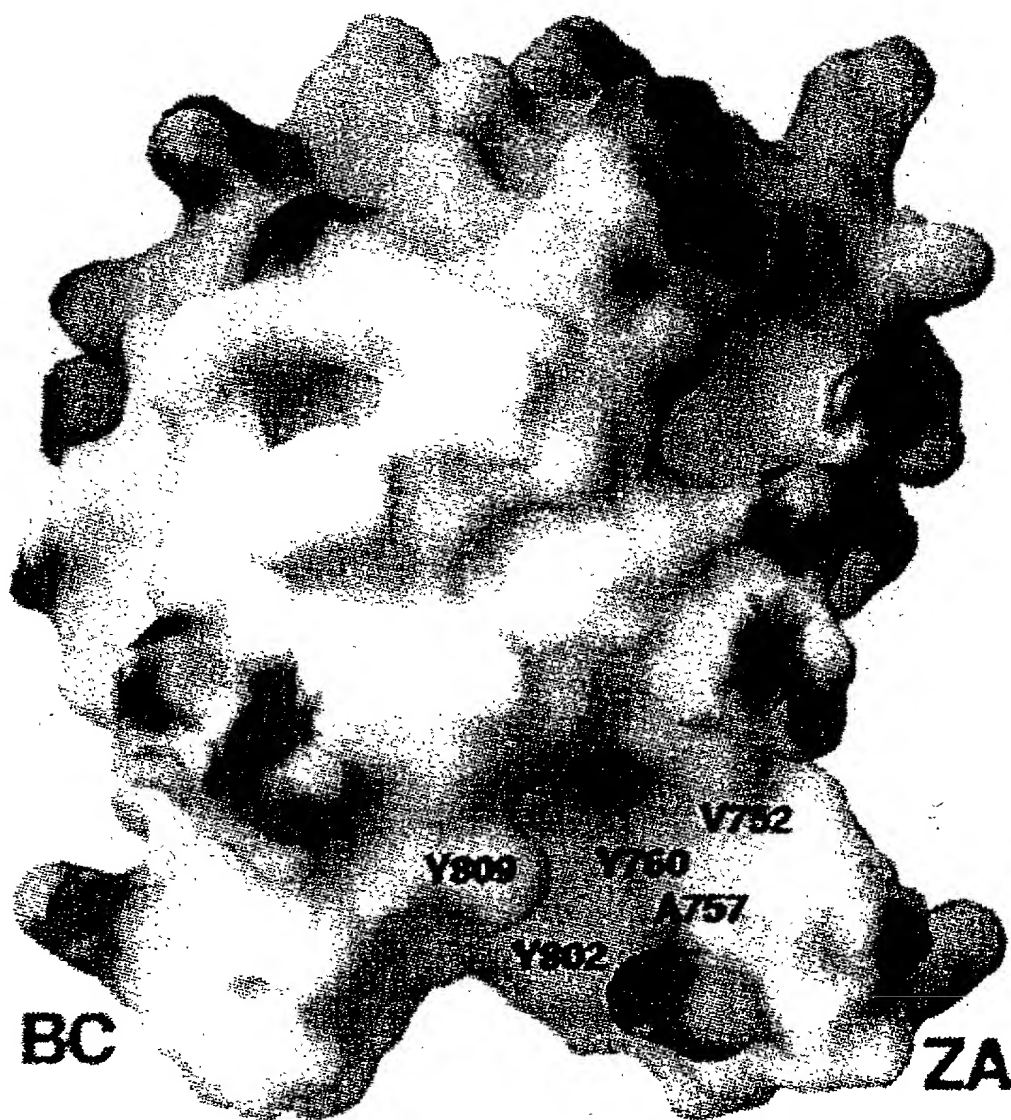


Figure 2H

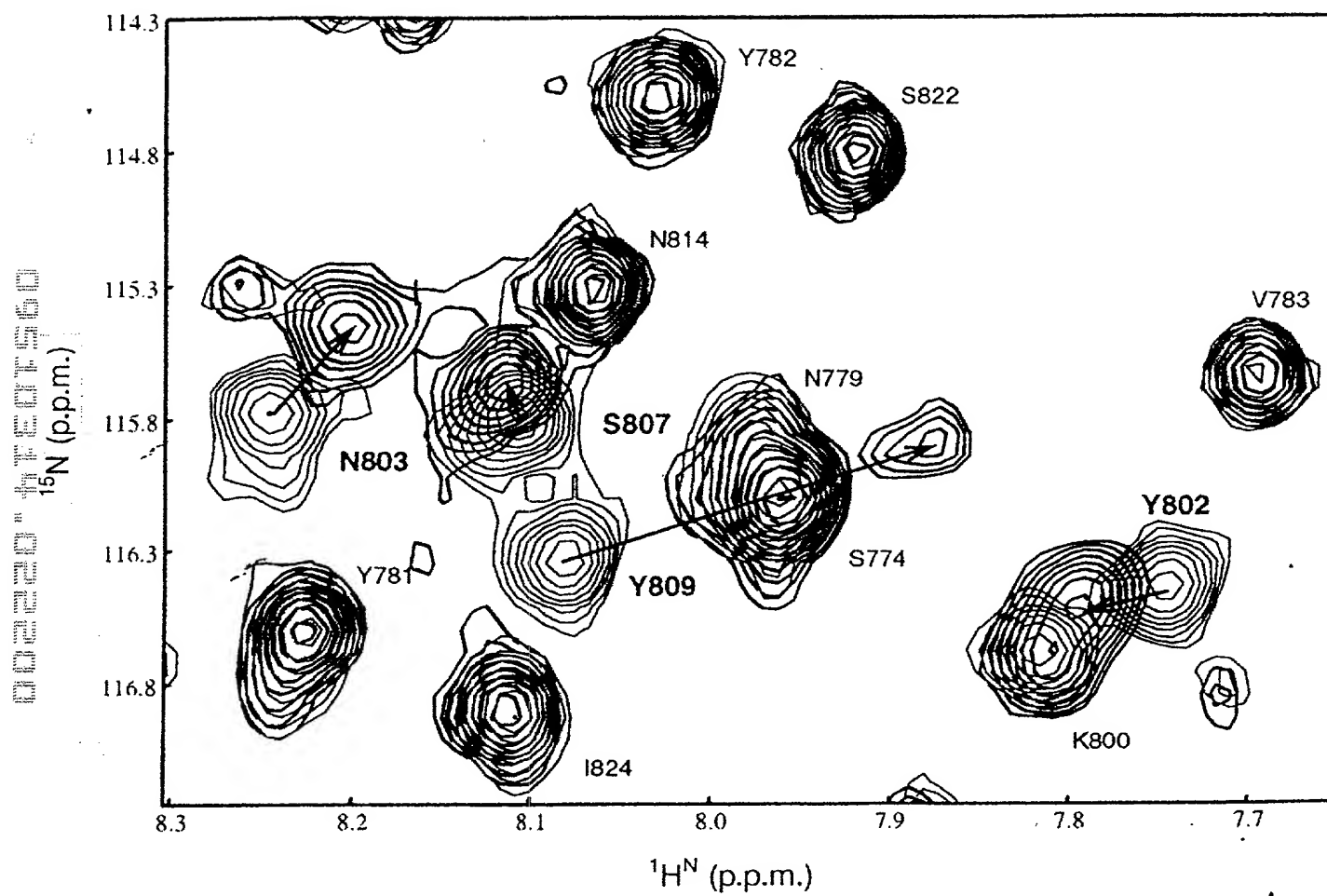


Figure 3A

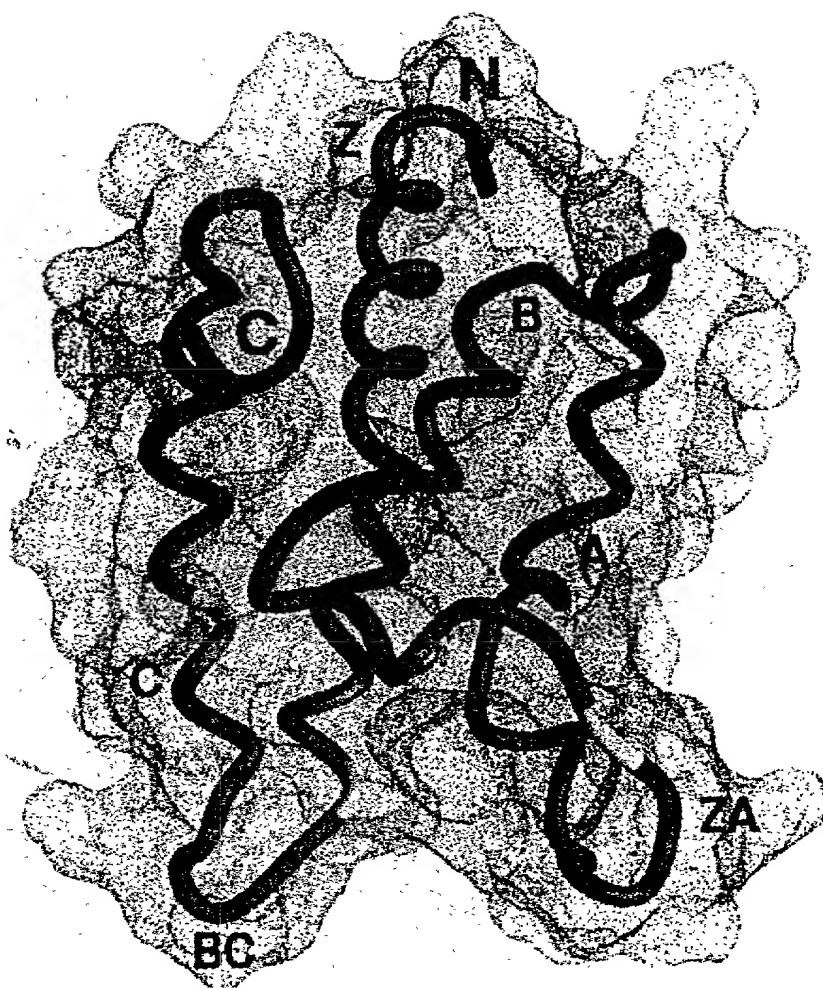
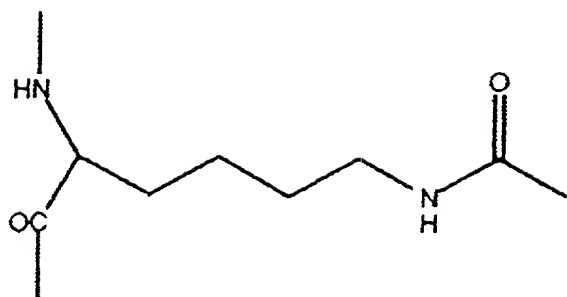
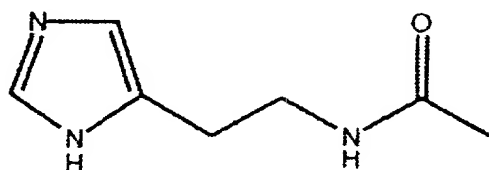


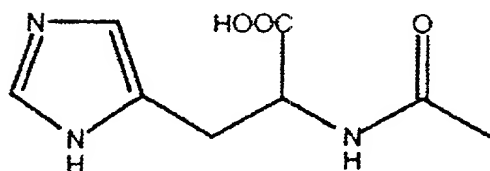
Figure 3B



Nε-acetyl-lysine



Nω-acetyl-histamine



Nα-acetyl-histidine

Figure 3C

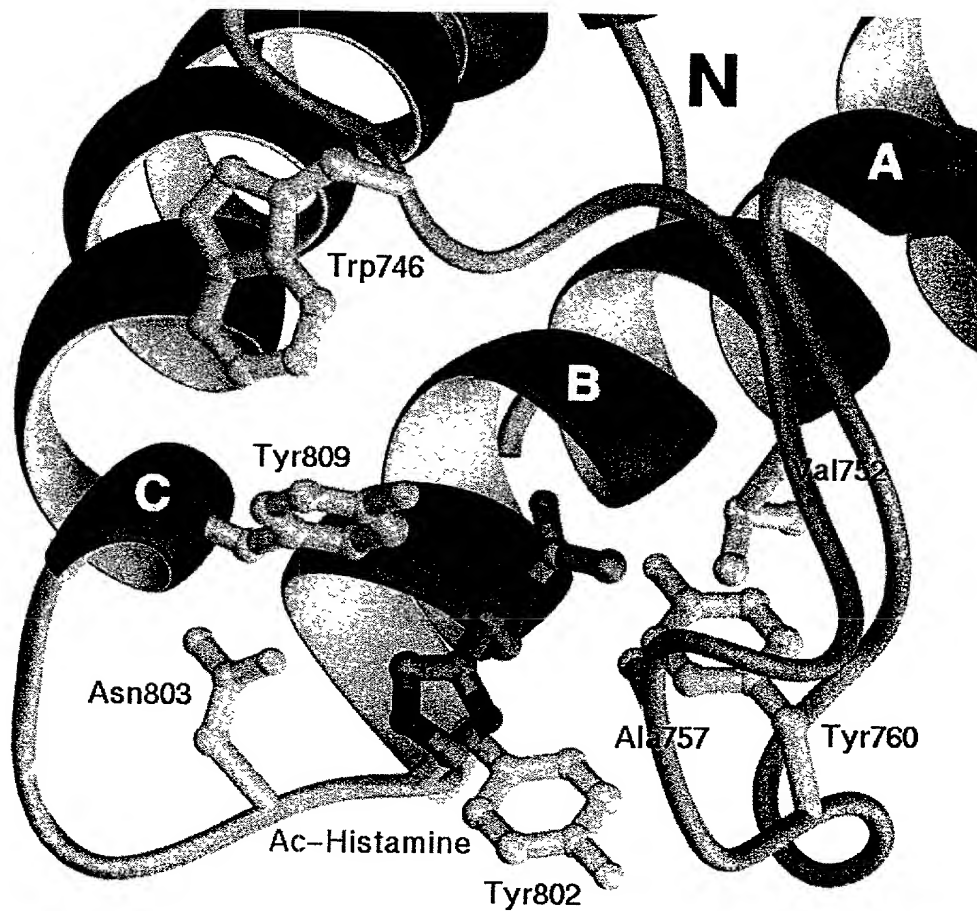


Figure 4

DECLARATION AND POWER OF ATTORNEY FOR PATENT APPLICATION

As below named inventors, we hereby declare that:

Our residence, post office address and citizenship are as stated below under our names.

We believe that we are the original, first and joint inventors of the subject matter which is claimed and for which a patent is sought on the invention entitled

METHODS OF IDENTIFYING MODULATORS OF BROMODOMAINS

the Specification of which

☒ is attached hereto
☐ was filed on _____
as Application Serial No. _____
and was amended on _____ (if applicable).

We hereby state that we have reviewed and understand the contents of the above-identified Specification, including the claims, as amended by any amendment referred to above.

We acknowledge the duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, 1.56(a).

We hereby claim foreign priority benefits under Title 35, United States Code, §119 of any provisional application filed in the United States in accordance with 35 U.S.C. §1.119(e), or any application for patent that has been converted to a Provisional Application within one (1) year of its filing date, or any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed.

PRIOR FILED APPLICATION(S)

<u>APPLICATION</u>	<u>COUNTRY</u>	<u>(DAY/MONTH/YEAR FILED)</u>	<u>PRIORITY</u>
<u>NUMBER</u>			<u>CLAIMED</u>

We hereby claim the benefit under Title 35, United States Code, §120 of any United States application listed below, and, insofar as the subject matter of each of the claims of this application is not disclosed in any prior United States application in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, §1.56(a), which occurred between the filing date of the prior application and the national or PCT international filing date of this application:

APPLICATION NO. _____ FILING DATE (DAY/MONTH/YEAR) _____ STATUS - PATENTED, PENDING, ABANDONED _____

We hereby appoint as our attorneys or agents the following persons: Stefan J. Klauber (Attorney, Registration No. 22,604); David A. Jackson (Attorney, Registration No. 26,742); Donald J. Cox, Jr. (Attorney, Registration No. 37,804); Michael D. Davis (Attorney, Registration No. 39,161); Allan H. Fried (Attorney, Registration No. 31,253); Christine E. Dietzel (Agent, Registration No. 37,309); and Michael A. Yamin (Agent, Registration No. P44,414), said attorneys or agents with full power of substitution and revocation to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

Please address all correspondence regarding this application to:

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HACKENSACK, NEW JERSEY 07601

Direct all telephone calls to David A. Jackson at (201) 487-5800.

We hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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Greenwich, CT 06870

SIGNATURE OF INVENTOR _____

DATE _____

DATE _____

SEQUENCE LISTING

<110> Zhou, Ming-Ming
Aggarnal, Aneel K

<120> METHODS OF IDENTIFYING MODULATORS OF BROMODOMAINS

<130> 2459-1-003

<140> UNASSIGNED

<141> 2000-02-22

<160> 44

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taattaaaga tggccgtggt attggtggta tctgtttccg tatgttccca tctcaaggat 2160
tcacagagat tgtcttctgt gctgtaacct caaatgagca agtcaaggcg tatggaacac 2220
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gtgagctaaa tccacggatc ccgtacacag aattttctgt catcattaaa aagcagaagg 2460
agataattaa aaaactgatt gaaagaaaac aggcacaaat tcgaaaagtt taccctggac 2520
tttcatgttt taaagatgga gttcgacaga ttcctataga aagcattcct ggaattagag 2580
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tcatggaacc tgtgaagaga acagaagtc caggatatta tgaagttata aggttcccca 2760
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tcatggcaga cttacagcga gtctttacca attgcaaaga gtacaacgcc gctgagagtg 2880
aatactacaa atgtgccaat atcctggaga aattcttctt cagtaaaatt aaggaagctg 2940
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gcctaaagca aggt 3014

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<210> 2

<211> 832

<212> PRT

<213> Homo sapiens

<400> 2

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Met Ser Glu Ala Gly Gly Ala Gly Pro Gly Gly Cys Gly Ala Gly Ala
  1             5             10            15

```

```

Gly Ala Gly Ala Gly Pro Gly Ala Leu Pro Pro Gln Pro Ala Ala Leu
      20             25             30

```

```

Pro Pro Ala Pro Pro Gln Gly Ser Pro Cys Ala Ala Ala Ala Gly Gly
      35             40             45

```

```

Ser Gly Ala Cys Gly Pro Ala Thr Ala Val Ala Ala Ala Gly Thr Ala
      50             55             60

```

```

Glu Gly Pro Gly Gly Gly Gly Ser Ala Arg Ile Ala Val Lys Lys Ala
      65             70             75             80

```

```

Gln Leu Arg Ser Ala Pro Arg Ala Lys Lys Leu Glu Lys Leu Gly Val

```


				85				90				95			
Tyr	Ser	Ala	Cys	Lys	Ala	Glu	Glu	Ser	Cys	Lys	Cys	Asn	Gly	Trp	Lys
100				105				110							
Asn	Pro	Asn	Pro	Ser	Pro	Thr	Pro	Pro	Arg	Ala	Asp	Leu	Gln	Gln	Ile
115				120				125							
Ile	Val	Ser	Leu	Thr	Glu	Ser	Cys	Arg	Ser	Cys	Ser	His	Ala	Leu	Ala
130				135				140							
Ala	His	Val	Ser	His	Leu	Glu	Asn	Val	Ser	Glu	Glu	Glu	Met	Asn	Arg
145				150				155				160			
Leu	Leu	Gly	Ile	Val	Leu	Asp	Val	Glu	Tyr	Leu	Phe	Thr	Cys	Val	His
165				170				175							
Lys	Glu	Glu	Asp	Ala	Asp	Thr	Lys	Gln	Val	Tyr	Phe	Tyr	Leu	Phe	Lys
180				185				190							
Leu	Leu	Arg	Lys	Ser	Ile	Leu	Gln	Arg	Gly	Lys	Pro	Val	Val	Glu	Gly
195				200				205							
Ser	Leu	Glu	Lys	Lys	Pro	Pro	Phe	Glu	Lys	Pro	Ser	Ile	Glu	Gln	Gly
210				215				220							
Val	Asn	Asn	Phe	Val	Gln	Tyr	Lys	Phe	Ser	His	Leu	Pro	Ala	Lys	Glu
225				230				235				240			
Arg	Gln	Thr	Ile	Val	Glu	Leu	Ala	Lys	Met	Phe	Leu	Asn	Arg	Ile	Asn
245				250				255							
Tyr	Trp	His	Leu	Glu	Ala	Pro	Ser	Gln	Arg	Arg	Leu	Arg	Ser	Pro	Asn
260				265				270							
Asp	Asp	Ile	Ser	Gly	Tyr	Lys	Glu	Asn	Tyr	Thr	Arg	Trp	Leu	Cys	Tyr
275				280				285							
Cys	Asn	Val	Pro	Gln	Phe	Cys	Asp	Ser	Leu	Pro	Arg	Tyr	Glu	Thr	Thr
290				295				300							
Gln	Val	Phe	Gly	Arg	Thr	Leu	Leu	Arg	Ser	Val	Phe	Thr	Val	Met	Arg
305				310				315				320			
Arg	Gln	Leu	Leu	Glu	Gln	Ala	Arg	Gln	Glu	Lys	Asp	Lys	Leu	Pro	Leu
325				330				335							
Glu	Lys	Arg	Thr	Leu	Ile	Leu	Thr	His	Phe	Pro	Lys	Phe	Leu	Ser	Met

<210> 3
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> VARIANT
<222> (2)
<223> It represents 2 to 3 undesignated amino acids.
They can be any amino acids.

<220>
<221> VARIANT
<222> (4)
<223> It represents 5 to 8 undesignated amino acids.
They can be any amino acids.

<220>
<221> VARIANT
<222> (6)
<223> It represents one undesignated amino acid. It can
be any amino acid.

<220>
<221> VARIANT
<222> (9)
<223> It represents 5 undesignated amino acids. They can
be any amino acids.

<220>
<221> VARIANT
<222> (5)
<223> It can be any amino acid from the group of: P, K,
or H.

<220>
<221> VARIANT
<222> (8)
<223> It can be any amino acid from the group of: Y, F,
or H.

<220>
<221> VARIANT
<222> (11)
<223> It can be any amino acid from the group of: M, I,

or V.

<400> 3

Phe Xaa Pro Xaa Xaa Xaa Tyr Xaa Xaa Pro Xaa Asp
1 5 10

<210> 4

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<220>

<221> SITE

<222> (6)

<223> It is acetyl-lysine.

<400> 4

Ile Ser Tyr Gly Arg Xaa Lys Arg Arg Gln Arg Arg
1 5 10

<210> 5

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<220>

<221> SITE

<222> (8)

<223> It is acetyl-lysine.

<400> 5

Ala Arg Lys Ser Thr Gly Gly Xaa Ala Pro Arg Lys Gln Leu
1 5 10

<210> 6

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<220>

<221> SITE

<222> (8)

<223> It is acetyl-lysine.

<400> 6

Gln Ser Thr Ser Arg His Lys Xaa Leu Met Phe Lys Thr Glu
1 5 10

<210> 7

<211> 110

<212> PRT

<213> Homo sapiens

<400> 7

Ser Lys Glu Pro Arg Asp Pro Asp Gln Leu Tyr Ser Thr Leu Lys Ser
1 5 10 15

Ile Leu Gln Gln Val Lys Ser His Gln Ser Ala Trp Pro Phe Met Glu
20 25 30

Pro Val Lys Arg Thr Glu Ala Pro Gly Tyr Tyr Glu Val Ile Arg Ser
35 40 45

Pro Met Asp Leu Lys Thr Met Ser Glu Arg Leu Lys Asn Arg Tyr Tyr
50 55 60

Val Ser Lys Lys Leu Phe Met Ala Asp Leu Gln Arg Val Phe Thr Asn
65 70 75 80

Cys Lys Glu Tyr Asn Ala Pro Glu Ser Glu Tyr Tyr Lys Cys Ala Asn
85 90 95

Ile Leu Glu Lys Phe Phe Phe Ser Lys Ile Lys Glu Ala Gly
100 105 110

<210> 8

<211> 110

<212> PRT

<213> Homo sapiens

<400> 8

Gly Lys Glu Leu Lys Asp Pro Asp Gln Leu Tyr Thr Thr Leu Lys Asn

<210> 10
 <211> 109
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 10
 Ala Gln Arg Pro Lys Arg Gly Pro His Asp Ala Ala Ile Gln Asn Ile
 1 5 10 15
 Leu Thr Glu Leu Gln Asn His Ala Ala Ala Trp Pro Phe Leu Gln Pro
 20 25 30
 Val Asn Lys Glu Glu Val Pro Asp Tyr Tyr Asp Phe Ile Lys Glu Pro
 35 40 45
 Met Asp Leu Ser Thr Met Glu Ile Lys Leu Glu Ser Asn Lys Tyr Gln
 50 55 60
 Lys Met Glu Asp Phe Ile Tyr Asp Ala Arg Leu Val Phe Asn Asn Cys
 65 70 75 80
 Arg Met Tyr Asn Gly Glu Asn Thr Ser Tyr Tyr Lys Tyr Ala Asn Arg
 85 90 95
 Leu Glu Lys Phe Phe Asn Asn Lys Val Lys Glu Ile Pro
 100 105

<210> 11
 <211> 112
 <212> PRT
 <213> *Homo sapiens*

<400> 11
 Lys Lys Ile Phe Lys Pro Glu Glu Leu Arg Gln Ala Leu Met Pro Thr
 1 5 10 15
 Leu Glu Ala Leu Tyr Arg Gln Asp Pro Glu Ser Leu Pro Phe Arg Gln
 20 25 30
 Pro Val Asp Pro Gln Leu Leu Gly Ile Pro Asp Tyr Phe Asp Ile Val
 35 40 45
 Lys Ser Pro Met Asp Leu Ser Thr Ile Lys Arg Lys Leu Asp Thr Gly
 50 55 60
 Gln Tyr Gln Glu Pro Trp Gln Tyr Val Asp Asp Ile Trp Leu Met Phe

002220" TFE0T560

<400> 13

Lys	Lys	Ile	Phe	Lys	Pro	Glu	Glu	Leu	Arg	Gln	Ala	Leu	Met	Pro	Thr
1				5					10					15	
Leu	Glu	Ala	Leu	Tyr	Arg	Gln	Asp	Pro	Glu	Ser	Leu	Pro	Phe	Arg	Gln
			20					25					30		
Pro	Val	Asp	Pro	Gln	Leu	Leu	Gly	Ile	Pro	Asp	Tyr	Phe	Asp	Ile	Val
		35					40					45			
Lys	Asn	Pro	Met	Asp	Leu	Ser	Thr	Ile	Lys	Arg	Lys	Leu	Asp	Thr	Gly
	50					55					60				
Gln	Tyr	Gln	Glu	Pro	Trp	Gln	Tyr	Val	Asp	Asp	Val	Arg	Leu	Met	Phe
65					70					75					80
Asn	Asn	Ala	Trp	Leu	Tyr	Asn	Arg	Lys	Thr	Ser	Arg	Val	Tyr	Lys	Phe
				85					90					95	
Cys	Ser	Lys	Leu	Ala	Glu	Val	Phe	Glu	Gln	Glu	Ile	Asp	Pro	Val	Met
			100					105					110		

<210> 14

<211> 111

<212> PRT

<213> Caenorhabditis elegans

<400> 14

Asp	Thr	Val	Phe	Ser	Gln	Glu	Asp	Leu	Ile	Lys	Phe	Leu	Leu	Pro	Val
1				5					10					15	
Trp	Glu	Lys	Leu	Asp	Lys	Ser	Glu	Asp	Ala	Ala	Pro	Phe	Arg	Val	Pro
			20					25					30		
Val	Asp	Ala	Lys	Leu	Leu	Asn	Ile	Pro	Asp	Tyr	His	Glu	Ile	Ile	Lys
		35					40					45			
Arg	Pro	Met	Asp	Leu	Glu	Thr	Val	His	Lys	Lys	Leu	Tyr	Ala	Gly	Gln
	50					55					60				
Tyr	Gln	Asn	Ala	Gly	Gln	Phe	Cys	Asp	Asp	Ile	Trp	Leu	Met	Leu	Asp
65					70					75					80
Asn	Ala	Trp	Leu	Tyr	Asn	Arg	Lys	Asn	Ser	Lys	Val	Tyr	Lys	Tyr	Gly

Pro Met Asp Leu Gln Thr Leu Arg Glu Asn Val Arg Lys Arg Leu Tyr
 50 55 60

Pro Ser Arg Glu Glu Phe Arg Glu His Leu Glu Leu Ile Val Lys Asn
 65 70 75 80

Ser Ala Thr Tyr Asn Gly Pro Lys His Ser Leu Thr Gln Ile Ser Gln
 85 90 95

Ser Met Leu Asp Leu Cys Asp Glu Lys Leu Lys Glu Lys Glu
 100 105 110

<210> 17

<211> 111

<212> PRT

<213> Homo sapiens

<400> 17

Leu Leu Asp Asp Asp Asp Gln Val Ala Phe Ser Phe Ile Leu Asp Asn
 1 5 10 15

Ile Val Thr Gln Lys Met Met Ala Val Pro Asp Ser Trp Pro Phe His
 20 25 30

His Pro Val Asn Lys Lys Phe Val Pro Asp Tyr Tyr Lys Val Ile Val
 35 40 45

Asn Pro Met Asp Leu Glu Thr Ile Arg Lys Asn Ile Ser Lys His Lys
 50 55 60

Tyr Gln Ser Arg Glu Ser Phe Leu Asp Asp Val Asn Leu Ile Leu Ala
 65 70 75 80

Asn Ser Val Lys Tyr Asn Gly Pro Glu Ser Gln Tyr Thr Lys Thr Ala
 85 90 95

Gln Glu Ile Val Asn Val Cys Tyr Gln Thr Leu Thr Glu Tyr Asp
 100 105 110

<210> 18

<211> 111

<212> PRT

<213> Mesocricetus auratus

<400> 18

Leu Leu Asp Asp Asp Asp Gln Val Ala Phe Ser Phe Ile Leu Asp Asn
 1 5 10 15

Ile Val Thr Gln Lys Met Met Ala Val Pro Asp Ser Trp Pro Phe His
 20 25 30

His Pro Val Asn Lys Lys Phe Val Pro Asp Tyr Tyr Lys Val Ile Val
 35 40 45

Ser Pro Met Asp Leu Glu Thr Ile Arg Lys Asn Ile Ser Lys His Lys
 50 55 60

Tyr Gln Ser Arg Glu Ser Phe Leu Asp Asp Val Asn Leu Ile Leu Ala
 65 70 75 80

Asn Ser Val Lys Tyr Asn Gly Ser Glu Ser Gln Tyr Thr Lys Thr Ala
 85 90 95

Gln Glu Ile Val Asn Val Cys Tyr Gln Thr Leu Thr Glu Tyr Asp
 100 105 110

<210> 19

<211> 111

<212> PRT

<213> Homo sapiens

<400> 19

Lys Pro Gly Arg Val Thr Asn Gln Leu Gln Tyr Leu His Lys Val Val
 1 5 10 15

Met Lys Ala Leu Trp Lys His Gln Phe Ala Trp Pro Phe Arg Gln Pro
 20 25 30

Val Asp Ala Val Lys Leu Gly Leu Pro Asp Tyr His Lys Ile Ile Lys
 35 40 45

Gln Pro Met Asp Met Gly Thr Ile Lys Arg Arg Leu Glu Asn Asn Tyr
 50 55 60

Tyr Trp Ala Ala Ser Glu Cys Met Gln Asp Phe Asn Thr Met Phe Thr
 65 70 75 80

Asn Cys Tyr Ile Tyr Asn Lys Pro Thr Asp Asp Ile Val Leu Met Ala
 85 90 95

Gln Thr Leu Glu Lys Ile Phe Leu Gln Lys Val Ala Ser Met Pro
 100 105 110

	20							25							30
Lys	Pro	Val	Asp	Ala	Ser	Ala	Leu	Gly	Leu	His	Asp	Tyr	His	Asp	Ile
	35						40					45			
Ile	Lys	His	Pro	Met	Asp	Leu	Ser	Thr	Val	Lys	Arg	Lys	Met	Glu	Asn
	50					55					60				
Arg	Asp	Tyr	Arg	Asp	Ala	Gln	Glu	Phe	Ala	Ala	Asp	Val	Arg	Leu	Met
	65				70					75				80	
Phe	Ser	Asn	Cys	Tyr	Lys	Tyr	Asn	Pro	Pro	Asp	His	Asp	Val	Val	Ala
				85					90					95	
Met	Ala	Arg	Lys	Leu	Gln	Asp	Val	Phe	Glu	Phe	Arg	Tyr	Ala	Lys	Met
			100					105						110	

Pro

<210> 24
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 24
Lys Lys Gly Lys Leu Ser Glu His Leu Arg Tyr Cys Asp Ser Ile Leu
1 5 10 15
Arg Glu Met Leu Ser Lys Lys His Ala Ala Tyr Ala Trp Pro Phe Tyr
20 25 30
Lys Pro Val Asp Ala Glu Ala Leu Glu Leu His Asp Tyr His Asp Ile
35 40 45
Ile Lys His Pro Met Asp Leu Ser Thr Val Lys Arg Lys Met Asp Gly
50 55 60
Arg Glu Tyr Pro Asp Ala Gln Gly Phe Ala Ala Asp Val Arg Leu Met
65 70 75 80
Phe Ser Asn Cys Tyr Lys Tyr Asn Pro Pro Asp His Glu Val Val Ala
85 90 95
Met Ala Arg Lys Leu Gln Asp Val Phe Glu Met Arg Phe Ala Lys Met
100 105 110

Figure 1 consists of 12 bar charts, each representing a different reason for leaving school. The x-axis for all charts represents age groups: 18-24, 25-34, 35-44, 45-54, 55-64, and 65+. The y-axis represents the percentage of respondents, ranging from 0 to 100. The categories are as follows:

- Most important reason for leaving school
- Reason for leaving school
- Reason for leaving school
- Reason for leaving school
- Reason for leaving school
- Reason for leaving school
- Reason for leaving school
- Reason for leaving school
- Reason for leaving school
- Reason for leaving school
- Reason for leaving school
- Reason for leaving school

The charts show varying trends across age groups. For example, in the first chart, the percentage of respondents who cite 'Financial reasons' as the most important reason increases with age, while in the second chart, the percentage of respondents who cite 'Lack of interest' as a reason for leaving school decreases with age.

```

<400> 25
Asn Lys Glu Lys Leu Ser Asp Ala Leu Lys Ser Cys Asn Glu Ile Leu
  1                               10                      15

Lys Glu Leu Phe Ser Lys Lys His Ser Gly Tyr Ala Trp Pro Phe Tyr
    20                               25                      30

Lys Pro Val Asp Ala Glu Met Leu Gly Leu His Asp Tyr His Asp Ile
    35                               40                      45

Ile Lys Lys Pro Met Asp Leu Gly Thr Val Lys Arg Lys Met Asp Asn
    50                               55                      60

Arg Glu Tyr Lys Ser Ala Pro Glu Phe Ala Ala Asp Val Arg Leu Ile
    65                               70                      75

Phe Thr Asn Cys Tyr Lys Tyr Asn Pro Pro Asp His Asp Val Val Ala
    85                               90                      95

Met Gly Arg Lys Leu Gln Asp Val Phe Glu Met Arg Tyr Ala Asn Ile
    100                              105                      110

```

```
<210> 26
<211> 113
<212> PRT
<213> Saccharomyces cerevisiae
```

19

35 40 45
 Val Lys Glu Pro Met Asp Leu Gly Thr Ile Ala Lys Lys Leu Asn Asp
 50 55 60
 Trp Gln Tyr Gln Thr Met Glu Asp Phe Glu Arg Glu Val Arg Leu Val
 65 70 75 80
 Phe Lys Asn Cys Tyr Thr Phe Asn Pro Asp Gly Thr Ile Val Asn Met
 85 90 95
 Met Gly His Arg Leu Glu Glu Val Phe Asn Ser Lys Trp Ala Asp Arg
 100 105 110
 Pro

<210> 27
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 27
 Met Glu Met Gln Leu Thr Pro Phe Leu Ile Leu Leu Arg Lys Thr Leu
 1 5 10 15
 Glu Gln Leu Gln Glu Lys Asp Thr Gly Asn Ile Phe Ser Glu Pro Val
 20 25 30
 Pro Leu Ser Glu Val Pro Asp Tyr Leu Asp His Ile Lys Lys Pro Met
 35 40 45
 Asp Phe Phe Thr Met Lys Gln Asn Leu Glu Ala Tyr Arg Tyr Leu Asn
 50 55 60
 Phe Asp Asp Phe Glu Glu Asp Phe Asn Leu Ile Val Ser Asn Cys Leu
 65 70 75 80
 Lys Tyr Asn Ala Lys Asp Thr Ile Phe Tyr Arg Ala Ala Val Arg Leu
 85 90 95
 Arg Glu Gln Gly Gly Ala Val Val Arg Gln Ala Arg
 100 105

<210> 28
 <211> 113

<212> PRT
<213> Homo sapiens

<400> 28

Ser Glu Asp Gln Glu Ala Ile Gln Ala Gln Lys Ile Trp Lys Lys Ala
1 5 10 15

Ile Met Leu Val Trp Arg Ala Ala Ala Asn His Arg Tyr Ala Asn Val
20 25 30

Phe Leu Gln Pro Val Thr Asp Asp Ile Ala Pro Gly Tyr His Ser Ile
35 40 45

Val Gln Arg Pro Met Asp Leu Ser Thr Ile Lys Lys Asn Ile Glu Asn
50 55 60

Gly Leu Ile Arg Ser Thr Ala Glu Phe Gln Arg Asp Ile Met Leu Met
65 70 75 80

Phe Gln Asn Ala Val Met Tyr Asn Ser Ser Asp His Asp Val Tyr His
85 90 95

Met Ala Val Glu Met Gln Arg Asp Val Leu Glu Gln Ile Gln Gln Phe
100 105 110

Leu

<210> 29
<211> 106
<212> PRT
<213> Gallus gallus

<400> 29

Asn Leu Pro Thr Val Asp Pro Ile Ala Val Cys His Glu Leu Tyr Asn
1 5 10 15

Thr Ile Arg Asp Tyr Lys Asp Glu Gln Gly Arg Leu Leu Cys Glu Leu
20 25 30

Phe Ile Arg Ala Pro Lys Arg Arg Asn Gln Pro Asp Tyr Tyr Glu Val
35 40 45

Val Ser Gln Pro Ile Asp Leu Met Lys Ile Gln Gln Lys Leu Lys Met
50 55 60

Glu Glu Tyr Asp Asp Val Asn Val Leu Thr Ala Asp Phe Gln Leu Leu

65		70		75		80									
Phe	Asn	Asn	Ala	Lys	Ala	Tyr	Tyr	Lys	Pro	Asp	Ser	Pro	Glu	Tyr	Lys
				85					90					95	

Ala	Ala	Cys	Lys	Leu	Trp	Glu	Leu	Tyr	Leu
			100					105	

<210> 30
 <211> 112
 <212> PRT
 <213> Gallus gallus

<400> 30
 Ser Ser Pro Gly Tyr Leu Lys Glu Ile Leu Glu Gln Leu Leu Glu Ala
 1 5 10 15

Val	Ala	Val	Ala	Thr	Asn	Pro	Ser	Gly	Arg	Leu	Ile	Ser	Glu	Leu	Phe
			20					25					30		

Gln	Lys	Leu	Pro	Ser	Lys	Val	Gln	Tyr	Pro	Asp	Tyr	Tyr	Ala	Ile	Ile
		35					40					45			

Lys	Glu	Pro	Ile	Asp	Leu	Lys	Thr	Ile	Ala	Gln	Arg	Ile	Gln	Asn	Gly
	50					55					60				

Thr	Tyr	Lys	Ser	Ile	His	Ala	Met	Ala	Lys	Asp	Ile	Asp	Leu	Leu	Ala
65					70					75					80

Lys	Asn	Ala	Lys	Thr	Tyr	Asn	Glu	Pro	Gly	Ser	Gln	Val	Phe	Lys	Asp
				85					90					95	

Ala	Asn	Ala	Ile	Lys	Lys	Ile	Phe	Asn	Met	Lys	Lys	Ala	Glu	Ile	Glu
			100					105					110		

<210> 31
 <211> 112
 <212> PRT
 <213> Gallus gallus

<400> 31
 Thr Ser Phe Met Asp Thr Ser Asn Pro Leu Tyr Gln Leu Tyr Asp Thr
 1 5 10 15

Val	Arg	Ser	Cys	Arg	Asn	Asn	Gln	Gly	Gln	Leu	Ile	Ser	Glu	Pro	Phe
			20					25					30		
Phe	Gln	Leu	Pro	Ser	Lys	Lys	Lys	Tyr	Pro	Asp	Tyr	Tyr	Gln	Gln	Ile
		35					40					45			
Lys	Thr	Pro	Ile	Ser	Leu	Gln	Gln	Ile	Arg	Ala	Lys	Leu	Lys	Asn	His
	50					55					60				
Glu	Tyr	Glu	Thr	Leu	Asp	Gln	Leu	Glu	Ala	Asp	Leu	Asn	Leu	Met	Phe
65					70					75					80
Glu	Asn	Ala	Lys	Arg	Tyr	Asn	Val	Pro	Asn	Ser	Ala	Ile	Tyr	Lys	Arg
				85					90					95	
Val	Leu	Lys	Met	Gln	Gln	Val	Met	Gln	Ala	Lys	Lys	Lys	Glu	Leu	Ala
			100					105					110		

<210> 32
 <211> 113
 <212> PRT
 <213> Gallus gallus

<400> 32															
Ser	Lys	Lys	Asn	Met	Arg	Lys	Gln	Arg	Met	Lys	Ile	Leu	Tyr	Asn	Ala
1				5					10					15	
Val	Leu	Glu	Ala	Arg	Glu	Ser	Gly	Thr	Gln	Arg	Arg	Leu	Cys	Asp	Leu
			20					25					30		
Phe	Met	Val	Lys	Pro	Ser	Lys	Lys	Asp	Tyr	Pro	Asp	Tyr	Tyr	Lys	Ile
		35					40					45			
Ile	Leu	Glu	Pro	Met	Asp	Leu	Lys	Met	Ile	Glu	His	Asn	Ile	Arg	Asn
	50						55				60				
Asp	Lys	Tyr	Val	Gly	Glu	Glu	Ala	Met	Ile	Asp	Asp	Met	Lys	Leu	Met
65					70					75					80
Phe	Arg	Asn	Ala	Arg	His	Tyr	Asn	Glu	Glu	Gly	Ser	Gln	Val	Tyr	Asn
				85					90					95	
Asp	Ala	His	Met	Leu	Glu	Lys	Ile	Leu	Lys	Glu	Lys	Arg	Lys	Glu	Leu

100 105 110

Gly

<210> 33
 <211> 115
 <212> PRT
 <213> Gallus gallus

<400> 33
 Lys Lys Ser Lys Tyr Met Thr Pro Met Gln Gln Lys Leu Asn Glu Val
 1 5 10 15
 Tyr Glu Ala Val Lys Asn Tyr Thr Asp Lys Arg Gly Arg Arg Leu Ser
 20 25 30
 Ala Ile Phe Leu Arg Leu Pro Ser Arg Ser Glu Leu Pro Asp Tyr Tyr
 35 40 45
 Ile Thr Ile Lys Lys Pro Val Asp Met Glu Lys Ile Arg Ser His Met
 50 55 60
 Met Ala Asn Lys Tyr Gln Asp Ile Asp Ser Met Val Glu Asp Phe Val
 65 70 75 80
 Met Met Phe Asn Asn Ala Cys Thr Tyr Asn Glu Pro Glu Ser Leu Ile
 85 90 95
 Tyr Lys Asp Ala Leu Val Leu His Lys Val Leu Leu Glu Thr Arg Arg
 100 105 110
 Glu Ile Glu
 115

<210> 34
 <211> 112
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism: Cited from
 Jeanmougin et al., Trends in Biochemical Sciences,
 22:151-153 (1997)

<400> 34

His Asn Ala Pro Phe Asp Lys Thr Lys Phe Asp Glu Val Leu Glu Ala
 1 5 10 15
 Leu Val Gly Leu Lys Asp Asn Glu Gly Asn Pro Phe Asp Asp Ile Phe
 20 25 30
 Glu Glu Leu Pro Ser Lys Arg Tyr Phe Pro Asp Tyr Tyr Gln Ile Ile
 35 40 45
 Gln Lys Pro Ile Cys Tyr Lys Met Met Arg Asn Lys Ala Lys Thr Gly
 50 55 60
 Lys Tyr Leu Ser Met Gly Asp Phe Tyr Asp Asp Ile Arg Leu Met Val
 65 70 75 80
 Ser Asn Ala Gln Thr Tyr Asn Met Pro Gly Ser Leu Val Tyr Glu Cys
 85 90 95
 Ser Val Leu Ile Ala Asn Thr Ala Asn Ser Leu Glu Ser Lys Asp Gly
 100 105 110

<210> 35

<211> 113

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: Cited from
 Jeanmougin et al., Trends in Biochemical Sciences,
 22:151-153 (1997)

<400> 35

Gly Thr Asn Glu Ile Asp Val Pro Lys Val Ile Gln Asn Ile Leu Asp
 1 5 10 15
 Ala Leu His Glu Glu Lys Asp Glu Gln Gly Arg Phe Leu Ile Asp Ile
 20 25 30
 Phe Ile Asp Leu Pro Ser Lys Arg Leu Tyr Pro Asp Tyr Tyr Glu Ile
 35 40 45
 Ile Lys Ser Pro Met Thr Ile Lys Met Leu Glu Lys Arg Phe Lys Lys
 50 55 60

<400> 37

Ser Pro Asn Pro Pro Asn Leu Thr Lys Lys Met Lys Lys Ile Val Asp
1 5 10 15

Ala Val Ile Lys Tyr Lys Asp Ser Ser Ser Gly Arg Gln Leu Ser Glu
20 25 30

Val Phe Ile Gln Leu Pro Ser Arg Lys Glu Leu Pro Glu Tyr Tyr Glu
35 40 45

Leu Ile Arg Lys Pro Val Asp Phe Lys Lys Ile Lys Glu Arg Ile Arg
50 55 60

Asn His Lys Tyr Arg Ser Leu Asn Asp Leu Glu Lys Asp Val Met Leu
65 70 75 80

Leu Cys Gln Asn Ala Gln Thr Phe Asn Leu Glu Gly Ser Leu Ile Tyr
85 90 95

Glu Asp Ser Ile Val Leu Gln Ser Val Phe Thr Ser Val Arg Gln Lys
100 105 110

Ile Glu

<210> 38

<211> 113

<212> PRT

<213> Gallus gallus

<400> 38

Ser Pro Asn Pro Pro Lys Leu Thr Lys Gln Met Asn Ala Ile Ile Asp
1 5 10 15

Thr Val Ile Asn Tyr Lys Asp Ser Ser Gly Arg Gln Leu Ser Glu Val
20 25 30

Phe Ile Gln Leu Pro Ser Arg Lys Glu Leu Pro Glu Tyr Tyr Glu Leu
35 40 45

Ile Arg Lys Pro Val Asp Phe Lys Lys Ile Lys Glu Arg Ile Arg Asn
50 55 60

His Lys Tyr Arg Ser Leu Gly Asp Leu Glu Lys Asp Val Met Leu Leu
65 70 75 80

Cys His Asn Ala Gln Thr Phe Asn Leu Glu Gly Ser Gln Ile Tyr Glu
85 90 95

Asp Ser Ile Val Leu Gln Ser Val Phe Lys Ser Ala Arg Gln Lys Ile
100 105 110

Ala

<210> 39
<211> 114
<212> PRT
<213> Gallus gallus

<400> 39
Ser Pro Asn Pro Pro Asn Leu Thr Lys Lys Met Lys Lys Ile Val Asp
1 5 10 15

Ala Val Ile Lys Tyr Lys Asp Ser Ser Ser Gly Arg Gln Leu Ser Glu
20 25 30

Val Phe Ile Gln Leu Pro Ser Arg Lys Glu Leu Pro Glu Tyr Tyr Glu
35 40 45

Leu Ile Arg Lys Pro Val Asp Phe Lys Lys Ile Lys Glu Arg Ile Arg
50 55 60

Asn His Lys Tyr Arg Ser Leu Asn Asp Leu Glu Lys Asp Val Met Leu
65 70 75 80

Leu Cys Gln Asn Ala Gln Thr Phe Asn Leu Glu Val Ser Leu Ile Tyr
85 90 95

Glu Asp Ser Ile Val Leu Gln Ser Val Phe Thr Ser Val Arg Gln Lys
100 105 110

Ile Glu

<210> 40
<211> 105
<212> PRT
<213> Homo sapiens

<400> 40
Ala Lys Leu Ser Pro Ala Asn Gln Arg Lys Cys Glu Arg Val Leu Leu

1	5	10	15
Ala Leu Phe Cys His Glu Pro Cys Arg Pro Leu His Gln Leu Ala Thr	20	25	30
Asp Ser Thr Phe Ser Leu Asp Gln Pro Gly Gly Thr Leu Asp Leu Thr	35	40	45
Leu Ile Arg Ala Arg Leu Gln Glu Lys Leu Ser Pro Pro Tyr Ser Ser	50	55	60
Pro Gln Glu Phe Ala Gln Asp Val Gly Arg Met Phe Lys Gln Phe Asn	65	70	75
Lys Leu Thr Glu Asp Lys Ala Asp Val Gln Ser Ile Ile Gly Leu Gln	85	90	95
Arg Phe Phe Glu Thr Arg Met Asn Glu	100	105	

<210> 41
 <211> 105
 <212> PRT
 <213> Mus musculus

<400> 41

Ala Lys Leu Ser Pro Ala Asn Gln Arg Lys Cys Glu Arg Val Leu Leu	1	5	10	15
Ala Leu Phe Cys His Glu Pro Cys Arg Pro Leu His Gln Leu Ala Thr	20	25	30	
Asp Ser Thr Phe Ser Met Glu Gln Pro Gly Gly Thr Leu Asp Leu Thr	35	40	45	
Leu Ile Arg Ala Arg Leu Gln Glu Lys Leu Ser Pro Pro Tyr Ser Ser	50	55	60	
Pro Gln Glu Phe Ala Gln Asp Val Gly Arg Met Phe Lys Gln Phe Asn	65	70	75	80
Lys Leu Thr Glu Asp Lys Ala Asp Val Gln Ser Ile Ile Gly Leu Gln	85	90	95	
Arg Phe Phe Glu Thr Arg Met Asn Asp	100	105		

<210> 42
 <211> 108
 <212> PRT
 <213> Mus sp.

<400> 42
 Thr Lys Leu Thr Pro Ile Asp Lys Arg Lys Cys Glu Arg Leu Leu Leu
 1 5 10 15
 Phe Leu Tyr Cys His Glu Met Ser Leu Ala Phe Gln Asp Pro Val Pro
 20 25 30
 Leu Thr Val Pro Asp Tyr Tyr Lys Ile Ile Lys Asn Pro Met Asp Leu
 35 40 45
 Ser Thr Ile Lys Lys Arg Leu Gln Glu Asp Tyr Cys Met Tyr Thr Lys
 50 55 60
 Pro Glu Asp Phe Val Ala Asp Phe Arg Leu Ile Phe Gln Asn Cys Ala
 65 70 75 80
 Glu Phe Asn Glu Pro Asp Ser Glu Val Ala Asn Ala Gly Ile Lys Leu
 85 90 95
 Glu Ser Tyr Phe Glu Glu Leu Leu Lys Asn Leu Tyr
 100 105

<210> 43
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: consencus

<220>
 <221> VARIANT
 <222> (1)
 <223> It represents 2 amino acids. They can be any amino acids.

<220>
 <221> VARIANT
 <222> (3)
 <223> It represents 2 to 3 amino acids. They can be any amino acids.

<223> Description of Artificial Sequence: consencus

<400> 44

Trp Pro Phe Met Glu Pro Val Lys Arg Thr Glu Ala Pro Gly Tyr Tyr
1 5 10 15

Glu Val Ile Arg
20

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